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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AA150541
BF899559
BM046590
BE175577
AU126850
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BM045988 603625140

AA150541 z14401.s

BF899559 pM4-MT020

BM046590 603626666

BE175577 RC5-HT058

BE175577 RC5-HT058

BM126850 AU126850

BM048864 603623901

AN821105 nr87h08.y

AA150849 z144b01.r

AL603419 DKFZp686F

B1020428 CM3-MT029

BM12989 CM3-MT029

BM372179 CM4-BT032

BM753417 603026311
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ALIGNMENTS

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ятт	118.6	118.6	120.2	123.2	125	125.2	129.8	146.2	168	169.4	170.4	172.2	173.2	175	178.2	181.8	184	184.6	185.8	186.6	193.4	197.2	201.8	203.4	213.4	216.6	222.2
15.2	15.3	15.3	15.5	15.9	16.1	16.1	16.7	18.8	21.6	21.8	21.9	22.2	22.3	22.5	22.9	23.4	23.7	23.8	23.9	24.0	24.9	25.4	26.0	26.2	27.5	27.9	28.6
916	838	524	790	339	343	346	997	469	492	753	1073	209	858	676	848	352	1156	222	786	787	1208	917	536	720	821	824	770
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BM043090	AQ748776	AQ539831	BF038233	BF762292	AA031883	BF762329	BE563253	AA223122	AW298308	BE780380	BG325647	BF056044	AL515088	BG436729	BE546076	T71406	BG250320	в1025710	BI818469	BE745635	BM478250	AL529460	AA453916	BG681978	BM049457	BE548028	в1825012
	AU/48//0 HS_00/0810		60145376			BF/62329 ILZ=CS004		AAZZ31ZZ ZTO6GOS.T	AW298308 UI-H-BWU-	_	BG32564 / 602424364	BF056044 /KU/910.X	AL515088 AL515088	~	BE5460/6 6010/24/8	T71406 yd35c10.ri	BG250320 602362453	CM3-MT02		60157871		₽		5679709 R	60362407	BE548028 5010/2055	

	REMARK	AUTHORS TITLE JOURNAL	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BC017852 LOCUS DEFINITION
Email: cgapbs-r@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Sequencing by: Sequencing Group at the Stanford Human Genome DNA Sequencing by: Sequencing Group at the Stanford, CA 94305 Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	<pre>Gene Collection (Mac), cancer behaviors Fifther M. 20892-2590, Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk</pre>	Strausberg,R.  Direct Submission Direct Submission Submitted (03-DEC-2001) National Institutes of Health, Mammalian Submitted (03-DEC-2001) National Institutes of Health, Mammalian	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1034)	mRNA. EC017852 BC017852.1 GI:17389657 HTC. human.	BC017852 1034 bp mRNA linear HTC 06-DEC-2001 Homo sapiens, tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain, clone IMAGE:4700855,

260 236.4 232.2 237.2

BM048564 AI1821105 AA150849 AL603419 BI020428 BI019989 AW372179 BI753417

FEATURES

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov series: IRAL Plate: 36 Row: p Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835042 This clone has the following problem: frame shifted.

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RESULT 2
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                                                    CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGA
                                                                                                          9cccca9ct9ct9aagagacaatgaccaccagcccggggactcctgcctcttctcattac
                                                                                                                                                                                    GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCGGGGACTCCTGCCTCTTCTCATTAC
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                                                                                                                                        AGCCCGGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACCCAGCCCGGGGACTCCT
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/clone_lib="NIH_MGC_77"
/lab_host="DH10B"
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/clone="IMAGE:4700855"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="LocusID:8794"
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                                                                                                                                                                                                                                                           262 tgtacagtttgtaaatcagatcaaaaacataaaagttcctgcaccatgaccagagacaca 321
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atgaacaccagcccggggactcctgccccagctgctgaagagacaatgaacaccagccca
                                                cagtgtgttgaagaatttggtgccaatgccactgtggaaaccccagctgctgaagagaca
                                                                                                                                                                             GTGTGTCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACTCCCCAGAGATGTGCCGGAAG
                                                                                                                                                                                                gtgtgtcagtgtaaagaaggcaccttccggaatgaaaactccccagagatgtgccggaag 381
                                                                                                                                                                                                                                            TGTACAGTTTGTAAATCAGATCAAAAACATAAAAGTTCCTGCACCATGACCAGAGACACA 393
                                                                                                               TGTAGCAGGTGCCCTAGTGGGGAAGTCCAAGTCAGTAATTGTACGTCCTGGGATGATATC
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                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity on wrong Insert Length: 1212 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates;
1 (bases 1 to 452)
NCI-CGAP http://dx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length:
Seq primer: -4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rt Length: 1212 Std Error: 0.00 primer: -40m13 fwd. ET from Amersham quality sequence stop: 211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1406602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 6.1e-117;
Nicmatches 1;
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                                                       ATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCGTCGTCGCCGGTCCTGCCGCCA 258
                                                                                                                               497;
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602572889F1 NIH_MGC_77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1535 row: b column: 24
High quality sequence stop: 617.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih
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                                                                                                                                                Similarity
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                                                                                                                                                                                                                                             203
                                                                                                                                 Conservative
                                                                                                                                                                                                                                /Clone_lib="NIH_MCC_77"
//lab_host="DH10B (TI phage-resistant)"
//lab_host="DH10B (TI phage-resistant)"
//note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgttcggcc); Site_2: Sfil (ggccattatggcc); 5'.and
3' adaptors were used in cloning as follows: 5' adaptor :
sequence: 5'.CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'.ATTCTAGAGCCGAGGGGGGCGACATG-dT(3))BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4700855"
                                                                                                                                                  48.3%;
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IMAGE:4700855 5',
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                                                                                                                                                                                                                                                                                            http://image.llnl.gov
plate: LLCM1942 row: p column:
High quality sequence stop: 757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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/lab_host="DH10B (phage resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5451897"
                                                                                                                                                    /clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
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                                                         Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags cenome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                              AA150541 454 bp mrNA Z144b01.s1 Soares_pregnant_uterus_NbHPU IMAGE:504745 3' similar to contains Alu element_MSR1 repetitive element_; mrNA
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                                                                                                                                                                                            AA150541.1
EST.
                                      Contact: Wilson RK
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Mammalia; 1
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Email: est@vatson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
INSET Length: 1559 Std Error: 0.00
Consortium for for boothers
                                                                                                                BF899559
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Site_2: Eco RI; 1st strand cD
oligo(dT) primer [5'
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/db_xref="GDB:3809733"
/db_xref="taxon:9606"
/clone="IMAGE:504745"
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/sex="female"
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tgcaccatgaccagagacacagtgtgtcagtgt-aaagaaggcaccttccggaatgaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 428)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare-
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 427.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM4&t2=PM4*MT0201-
031200-002-c07&t3=2000-12-03&t4=1)
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.
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122 c 109 g
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/db_xref="taxon:9606"
/clone_lib="MT0201"
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426; Conser
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Plate: LLCM1946 row: c column:
High quality sequence stop: 737
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="carcinoma, cell line"
/lab_host="0H10B (phage resistant)"
/note="Organ: prostate; vector: poTB7; Site_1: XhoI;
Site_2: EcoRI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                             of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5453129"
/clone_lib="NIH_MGC_40"
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Pred. No. 6.1e-84;
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Catarrhini;
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i; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simpson, A.J.
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Eukaryota; Metazoa;
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BE175577
RC5-HT0580-100500-022-H09
BE175577
BE175577.1 GI:8638306
                                                                                                                                                                                                                                                         (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC5-HT0580-100
500-022-H09&t3=2000-05-10&t4=1),
                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence tags
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      108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natl. Acad.
    þ
Inote-"Organ: head_neck; vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0580"
                                                                                                                        /dev_stage="Adult"
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                                                                                                                                                                                                                                       Email: genomics@hri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                       Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812,
Tel: 81-438-52-3952
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Takao Isog
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                             HRI human cDNA project 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. an
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Mammalia; Eutheria;
1 (bases 1 to 538)
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                                                                                                                                                                                                                          Research Institute.
/cell_type="teratocarcinoma"
/cell_line="NT2"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal
/note="Vector: pweks retinoic acid (RA) induction
cells after 2-weeks retinoic acid (RA) induction
154 c 141 g 100 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                          Takao Isogai
                                                                                                     /clone="NT2RP2000080"
/clone_lib="NT2RP2"
                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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Pred. No. 1.4e-82;
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BM048564
BM048564.1 GI
                                                                                                                                                                                                                                          Plate: LLCM1937 row: b column: High quality sequence stop: 658. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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603623901F1 NIH_MGC_40
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http://image.llnl.gov
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/lab_host="DH10B (phage resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_ore="Taxon:9606"
/clone="IhAGE:5449633"
/clone_lib="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/tissue_type="carcinoma, cell line"
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AI821105

NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1175007 5'

SIMILIAR to TR:014755 014755 TRAIL RECEPTOR 3. [1] ;, mRNA sequence.
                                                                 Tissue Procurement: Suzanne L. Topalian, M.D., Ph.D.
                                                                                         Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.go
                                                                                                                  Unpublished (1997)
Other_ESTs: nr87h08.x5
                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
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cDNA Library Preparation: Stratagene, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         agcttactctgccaccactgcccggcaggaggaagttcccccagcagacagtggccccaca 125
                                                                                                                                                                             TGAGATGTGCTCGACGTGT 546
                                                                                                                                                                                                                             CACGACCAGAGACACCGTGTCAGTGGTGAAAAAGGAAGCTTNCAGGATAAAAACTGCCC
                                                                                                                                                                                                                                                                             GCCTTCTTGCCTGCTATGTACNAGTTTGTAATCAGGTCAAACAAATAAAAGTTCCTGTAC 467
                                                                                                                                                                                                                                                                                                                             TACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTT 407
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Z144b01.r1 So
IMAGE:504745
 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                          Homo sapiens
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                                                                                    Soares_pregnant_uterus_NbHPU
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85.5%;
 Chordata;
Primates;
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Craniata; V
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ches 55;
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                                                                                                 Homo sapiens
             Vertebrata;
 Hominidae;
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              Euteleostomi;
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DEFINITION

AL603419 462 bp mRNA DKFZp686F087\_rl 686 (synonym: hlcc3) Homo

sapiens

linear

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                                                                 AATGAACCTTCTTGCTTCCCATGTAC
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore

AB., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,

Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

Geheration and analysis of 280,000 human expressed sequence tags

Gendmer Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email:\est@watson.wustl.edu
This chone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
Insert Length: 1559 Std Error: 0.00
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Organ: uterus; Vector: pT7T3-Pac; Site, Eco RI; 1st strand cDNA was primed with primer [5', A&AATTCGCGGCCGCCTTTTTTTTTTTTTTTTTT 3']
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tranded cDNA was ligated to Eco RI adaptors a), digested with Not I and cloned into the No. Il sites of the modified pT7T3 vector. Library uigh one round of normalization. Library ed by M. Fatima Bonaldo."
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Pred.
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No. 1e-63;
                                                                                                                                                                                                                                                                                 GAGGGAAGTTCCCCAGCAGACAGTGGCC
                                                                                                                                                  tgtggattacaccaacgcttccaac 240
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                                                                                                                                  GATTACACCAACGCTTCCAAC
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DKFZp686F087

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            BI020429

CM3-MT0392-120101-616-d05

BI020428

BI020428.1 GI:14427058

EST.
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Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@tktz-heidelberg.de; sequenced by EMBL (European Molecular Biology Labboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l (bases 1 to 462)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S. EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wie Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
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human
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Mammalia; Eutheria;
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cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_ore="DKRZp666F087"
/clone_lib="686 (synonym: hlo
/tissue_type="human skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B"
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MT0292 Homo sapiens cDNA,
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                        aagtccaagtcagtaattgt 423
                                                                                                              ccttccggaatgaaaactccccagagatgtgccggaagtgtagcaggtgccctagtgggg 403
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AAGTCCAAGTCAGTAATTGT
                                                                                                                                                                                                                                                                                                                                                                   CAGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATT 284
                                                                                      CCTTCCGGAATGAAAACTCCCCAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGGGG
                                                                                                                                                                                                                                                                          ACACCAACGCTTCCAACAATGAACCTTCTTGCTTCCCATGTACAGTTTGTAAATCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0292-
120101-616-d05&t3=2001-01-12&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
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1 (bases 1 to 484)

Dias Neto, E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare',

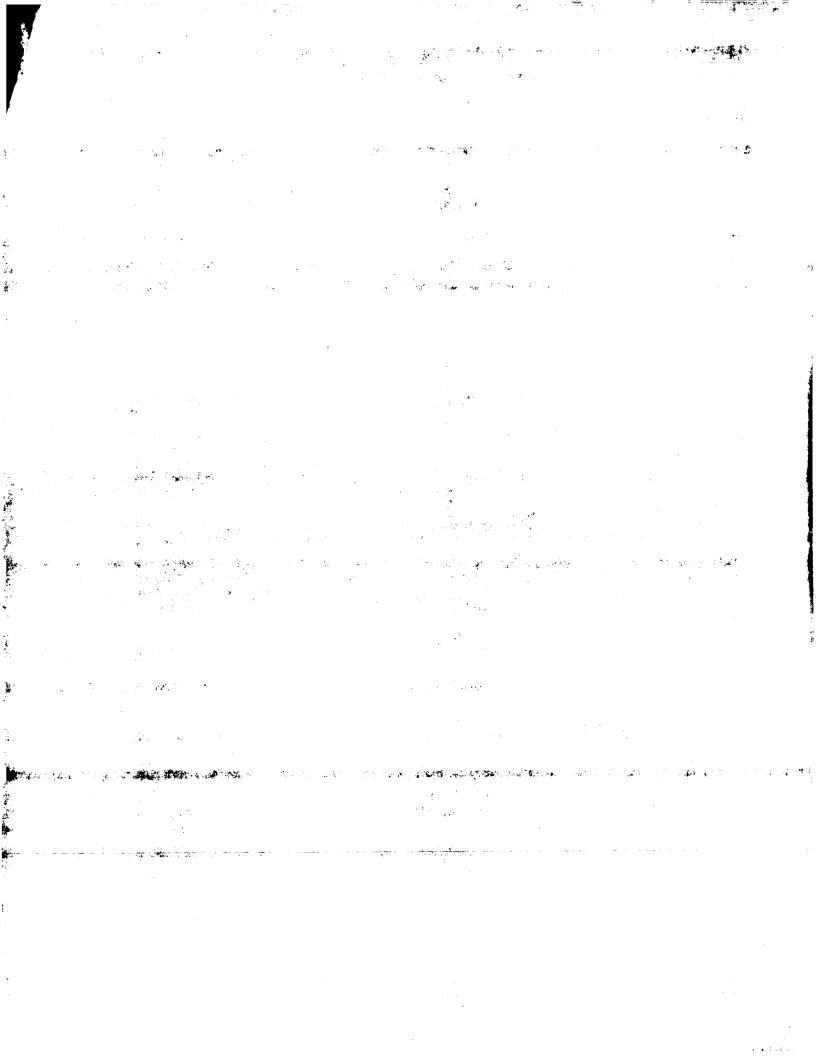
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Adult"
/note="organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
/note="organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 19, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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/db_xref="taxon:9606"
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Pred. No. 6.7e-63;
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Best Local Similarity
Matches 237; Conserv
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224 acaccaacgcttccaacaatgaaccttcttgcttcccatgtacagtttgtaaatcagatc 283
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                                                                                     AAAAACATAAAAGTTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCCA 350
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3st2=CM3-MT0292-
110101-625-609st3=2001-01-11st4-1)
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Dias Neto, E.,
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+55-11-2707001
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                        Score 236.4; DB 10;
Pred. No. 3.1e-56;
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Search completed: August 13, 2002, 10:49:52 Job time: 8456 sec



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US-09-006-353A-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BROCKES, ANDERS A
NAME: BROC
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5 NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: HUMAN
STREET: 9410 KEY
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
                                                                           LENGTH:
TYPE: a
                                                    TOPOLOGY:
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                                                                        amino acid
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                                                                                                  259 amino acids
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US-08-965-688-2
US-08-751-7673-2
US-09-260-173-2
US-09-272-796-7
US-09-180-827-7
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US-08-816-977-39
US-08-816-977-39
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US-08-816-977-39
US-08-816-217-7
US-08-816-217-7
US-08-816-217-7
US-08-816-913-84-84
US-08-818-283-4
US-08-983-0358-4
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Query Match

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Length

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US-09-153-927-3
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US-09-086-483A-2
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Best Local S
Matches 233
Sequence 2, Application US/09086483A Patent No. 6214580
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McDonnell, Peter C.
APPLICANT: Young, Peter R.
APPLICANT: Zou, Jun
TITLE OF INVENTION: A Method of Identifying Agonists and
TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1,
TITLE OF INVENTION: and TR5
FILE REFERENCE: GH50031
CURRENT APPLICATION NUMBER: US/09/153,927A
CURRENT FILING DATE: 1998-09-16
EARLIER FILING DATE: 1997-10-08
EARLIER FILING DATE: 1997-10-08
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nes 233; Conserv
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   HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
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Pred. No. 1.1e-234;
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

STREET: 9410 KEY CITY: ROCKVILLE

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ADDRESSEE:

E: HUMAN GENOME SCIENCES, 9410 KEY WEST AVENUE

COUNTRY:

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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                             APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: THE
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/19 PRIOR FILING DATE: 1997-05-09 PRIOR APPLICATION NUMBER: 60/0 PRIOR FILING DATE: 1997-03-14 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OURRENT APPLICATION NUMBER: US/09/U80, APPLICATION MAY-29-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/050,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 TGACNPCTEGVDYT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: DE CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                    60/041,230
                                                                    08/853,684
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; NAME/KEY: xaa
; LOCATION: 410
; OTHER INFORMATION: xaa = leu or met
US-09-329-633A-2
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US-09-329-633A-2
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Best Local Similarity
Matches 8; Conser
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 4
                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09079029 Patent No. 6342369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, K. Jin
APPLICANT: Kim, K. Jin
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY
FILE REFERENCE: P146R1 (REVISED)
CURRENT APPLICATION NUMBER: US/09/329,633A
CURRENT FILING DATE: 1990-06-10
PRIOR APPLICATION NUMBER: US 60/089,253
PRIOR FILING DATE: 1998-06-12
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 303
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 411
                                                                                                                                                                                               APPLICANT: Adams, Camilla W. APPLICANT: Ashkenazi, Avi J. APPLICANT: Chuntharapai, Anan APPLICANT: Kim, Kyung J.
                                                                                                                                                             APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                149 SPEMCRKC 156
                                                                      CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                  95 SPEMCRKC 102
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                                        COUNTRY: U
ZIP: 94080
                                                                                                         STREET:
                                                                                                                            ADDRESSEE:
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                                                                                                         1 DNA Way
                                                       USA
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                                                                                                                          Genentech, Inc
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100.0%; Pred. No.
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THE METHOD
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SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICATION NUMBER:

US/09/079,029

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RESULT 8
US-09-333-593A-8
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR APPLICATION NUMBER: 60/041,230
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NEC
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                               TYPE: PRT
ORGANISM: HOMO SAPIENS
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                                                                                                                                                                                                                                                LENGTH: 412
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REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                             149 SPEMCRKC 156
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                                                                            95 SPEMCRKC 102
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5. 6313269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MARSHALL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650/952-9881
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                                                                                                                         Conservative
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                                                                                                                        3.4%; Score 8;
100.0%; Pred. Notive 0; Misma
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                                                                                                                         Mismatches
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                                                                                                                                        NO.
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 8
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PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
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TITLE OF INVENTION:
FILE REFERENCE: GH-
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SOFTWARE: FastSEQ for Windows Version 3.0
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TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                              COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,036A
FILING DATE: 26-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                   APPLICATION NUMBER: US --to be assigned-
FILING DATE: 04-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,536
FILING DATE: 28-MAR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rauch, Charles
APPLICANT: Walczak, Henning
TITLE OF INVENTION: Receptor That Binds TRAIL
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 SPEMCRKC
APPLICATION NUMBER: US 0 FILING DATE: 12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle, STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 SPEMCRKC 102
                                                                                                                                                                                                                                                                                                                                           ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRUNEH, ALEMSEGED
VENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MARSHALL, LI
ROSHAK, AMY
                                                                                                                                                                                                                                                                                                                                                                                                                   E: Kathryn A. Anderson, Immunex Corporation 51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.4%; Score 8;
100.0%; Pred. No.
                   US 08/815,255
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US 08/799,861 FILING DATE: 13-FEB-1997

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; MOLECULE TYPE: protein US-08-883-036A-2
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US-08-465-380-61
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 233-064
TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                               TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: (
                                                                                FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 SPEMCRKC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2625-D
                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 90071
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633 West Fifth Street
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
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                                                                                                                                                                                                             08/326,110
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b; Pred. No. 2.3
0; Mismatches
                                                                                                                       213/268
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; MOLECULE TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Nec
US-08-486-397-61
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; ORIGINAL SOURCE:
; ORGANISM: Necator ame
US-08-465-380-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 61,
 Best Local Similarity
Matches 7; Conserv
                                     Query Match
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                                                                                                                                                                                                                                             TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326
FILING DATE: October 18, 1
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.I. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Larcoche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
STREET: Suite 4700
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 VCQCKEG 43
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                                                                                                                                                                                      amino acid
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3.0%; Score 7; DB 2; ilarity 100.0%; Pred. No. 3.7; Conservative 0; Mismatches
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                                     Length 61;
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RESULT 13
US-08-461-965-61
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US-08-486-399-61
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                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/
TELECOMBUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
Sequence 61, Application US/08461965 Patent No. 5872098
                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NUMBE: DECCE CULTARINEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: IBM P.C. SOFTWARE: WORD Perfect 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yannick G.J. Gar
APPLICANT: Peter W. Bergum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Loe
                                                                                           82 VCQCKEG
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37 VCQCKEG
                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08, FILING DATE: June 5, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37
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                                                                                                                                                                                                                                                                                                             amino acid
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California
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                                                                                                                                                                                                                                                                                                                             61 amino acids
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Joris H.L. Mensens, Marc J. Lauwereys,
Yves R. Laroche, Laurent S. Jespers,
Yannick G.J. Gansemans, Matthew Moyle,
                                                                                                                                                        larity 100.0%; F
Conservative 0;
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                                                                                                                                                                                                                                                                                peptide
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                                                                                                                                                                      Score 7; I
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      213/270
                                                                                                                                                                      DB 2;
                                                                                                                                                                                     Length 61;
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RESULT 14
US-08-634-641-61
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Best Local Similarity
7; Conserve
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US-08-461-965-61
                                                                                                                                                                                                 Sequence 61, Application US/08634641 Patent No. 5955294
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APPLICATION NUMBER: 08/326,11
EILING DATE: OCTOBER 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/
                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 61 amino acids
                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
TITLE OF INVENTION:
                                                                 APPLICANT:
                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                 82 VCQCKEG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 amino acids
                                                                                                                              Vlasuk, George P. Vlasuk
Stanssens, Patrick Eric Hugo
Mensens, Joris Hilda Lieven
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                                                                              Jespers, Laurent
                                                                                                               Lauwereys, Marc Josef
                                Bergum, Peter W.
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                              Moyle, Matthew
                                                               Gansemans, Yannick Georges Jozef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                 3.0%; Score 7; DB 2; 100.0%; Pred. No. 3.7;
NEMATODE-EXTRACTED ANTICOAGULANT PROTEIN
                                                                                                 Yves Rene
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er 18, 1994
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US-08-634-641-61
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TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
                                                                                                                                                        Sequence 61, Applicat Patent No. 6040441 GENERAL INFORMATION:
                                                                                                   GENERAL INFOR APPLICANT:
APPLICANT:
APPLICANT:
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Best Local 9
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FILING DATE: June 5,1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5,1995
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18,1994
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18,1994
APPLICATION NUMBER: 30,158
RESISTRATION NUMBER: 30,158
RESISTRATION NUMBER: 30,158
RESISTRATION NUMBER: 30,158
APPLICANT:
APPLICANT:
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APPLICANT:
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MOLECULE TYPE:
ORIGINAL SOURCE:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/6: FILING DATE: April 19, 1996 PRIOR APPLICATION DATA:
                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                37 VCQCKEG
                                                                                                                                                                                                                                                                                                    82 VCQCKEG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/13231 FILING DATE: October 17, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                   l Similarity
7; Conserv
                                                                                                                                                                          l, Application US/09249471
6040441
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California
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                Gansemans, Yannick Georges Jozef Moyle, Matthew
                                                  Laroche, Yves Rene
Jespers, Laurent Stephane
                                                                                                     Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
                                                                                                                                        Vlasuk, George Phillip
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                                                                                   Lauwereys, Marc Josef
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100.0%; Pred. No.
tive 0; Mismatc
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5. 3.7;
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US-09-249-472-61
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Best Local Similarity
"hes 7; Conserv?
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              GENERAL INFORMATION:
APPLICANT: Vlasuk,
APPLICANT: Stanssen
APPLICANT: Messens
                                                                                   Sequence 61, Application US/09249472 Patent No. 6046318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/132:
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS: LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
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APPLICANT:
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                                                                                                                                                                                                                                 82 VCQCKEG 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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633 West Fifth Street
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              Vlasuk, George Phillip
Stanssens, Patrick Eric Hugo
Messens, Joris Hilda Lieven
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Lauwereys, Marc Josef
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30,158
216/270
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RESULT 17
US-09-249-451-61
; Sequence 61, Application US/09249451
; Patent No. 6087487
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US-09-249-472-61
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
                                                                                                                                                                                            Best Local Similarity
Matches 7; Conserve
                                                                                                                                                                                                                                Query Match
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APPLICATION NUMBER: 08/809,455

FILING DATE: APril 17, 1997

APPLICATION NUMBER: PCT/US95/132:

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: TANK DO DOG 5 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/325,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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TITLE OF INVENTION:
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37 VCQCKEG 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Annol-
                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BIGGS, SUZANNI REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
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California
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100.0%; Pred. No.
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or 17, 1995
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5. 3.7;
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APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION NUMBER: 08/809,455
APPLICATION NUMBER: 08/809,455
FILING DATE: APRIL 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
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US-09-249-451-61
                                     Best Local Similarity
Matches 7; Conserv
                                                                           Query Match
                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                             NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: IBM P.C. SOFTMARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
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MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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APPLICATION NUMBER: 08/326,110
APPLICATION OCTOBER 18, 1994
82 VCQCKEG 88
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STREET: Suite 4700
CITY: Los Angeles
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                                       Conservative
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Jespers, Laurent Stephane
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Messens, Joris Hilda Lieven
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                                                         3.0%; Score 7; 1
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                                       0; Mismatches
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                                                         DB 3;
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                                       0;
                                                                           Length 61;
                                       Indels
                                       0
                                       Gaps
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VCQCKEG

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; MOLECULE TYPE: p
; ORIGINAL SOURCE:
; ORGANISM: Neca
US-08-809-455-61
Qy
                 Query Match
Best Local Similarity
Thes 7; Conserve
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Patent No. 6
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                                                                                                                                                                                                                                    TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: U0/-
APPLICATION NUMBER: U0/-
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
APPLICATION NUMBER: 08/465,380
TTT TNG DATE: June 5, 1995
TTT TNG DATE: 1995
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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TITLE OF
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APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: DATE: OCTOBERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/8 FILING DATE: April 17, 1997 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                    LENGTH: b1 cm.
mvpE: amino acid
mvpE: amino acid
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APPLICATION NUMBER: 08/405,...
FILING DATE: June 5, 1995
FILING DATE: 08/461,965
   82 VCQCKEG 88
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                        NAME: BIGGS, SUZANN REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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Los Angeles
E: California
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                                                                                                                                                                                                                      61 amino acids
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633 West Fifth Street
                                   Conservative
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Messens, Joris Hilda Lieven
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                                                                                                                                   Necator americanus
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                               3.0%; Score 7; DB 100.0%; Pred. No. 3. 100.0%; Pred. No. 3. 100.0%; Mismatches
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                                                                                                                                                                                                                                                                                                                                      216/270
                                                                Length 61;
                                 0; Indels
                               0
                               Gaps
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; MOLECULE TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Nec
US-09-249-461-61
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US-09-249-461-61
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                                                                                                                      TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                             FILING DATE: October 18, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,380
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: SULL.
STREET: Los Angeles
CTATE: California
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TITLE OF INVENTION:
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FILING DATE: April 17, 1997
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 7
                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                    NAME:
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                                                                                                     LENGTH:
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633 West Fifth
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Messens, Joris Hilda Lieven
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Gansemans, Yannick Georges Jozef
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Stanssens, Patrick Eric Hugo
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                                                                    linear
                  Necator americanus
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                                                                                                                                                                             955-0440
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Length 61;

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Best Local Similarity
Thehes 7; Conserv
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                                                                                              NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPA: (213) 489-1600
TELEPA: (213) 955-0440
TELEPA: 67-3510
INFORMATION FOR SEQ ID NO: 61:
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APPLICATION NUMBER: 08/809,455

FILING DATE: April 17, 1997

APPLICATION NUMBER: PCT/US95/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 3, 1994

APPLICATION NUMBER: 08/326,110

FILING DATE: JUNE 3, 1994

APPLICATION TUREDMATION.
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APPLICANT: Moyle, Ma
APPLICANT: Bergum, F
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                       SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE 1.
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STATE: California
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STREET: 633 West Fifth Street
STREET: Suite 4700
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                           TOPOLOGY:
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        TYPE:
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Messens, Joris Hilda Lieven
Lauwereys, Marc Josef
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                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
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PCT-US93-08528-335; Sequence 335, Application PC/TUS9308528; GENERAL INFORMATION:
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; ORGANISM: Nec
US-09-249-448-61
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                                                                        Best
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Patent No. 5508384
                                                          Matches
                                                                                      Query Match
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Best Local
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                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
                                                                                                                                              STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01 FILING DATE: 09-SEP-1993 PRIOR APPLICATION DATA:
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APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                           TELLEFAX: 201
TELLEFAX: 248633
                           225 LIVLLIV 231
                                                       Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                                                                                 NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,033 REFERENCE/DOCKET NUMBER: MU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 7; Conserv
9 LIVLLIV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 VCQCKEG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 VCQCKEG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08118270
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                                                         3.0%; Score 7; DB 1; ilarity 100.0%; Pred. No. 5.6; Conservative 0; Mismatches
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                                                                                     Length 93;
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     9 LIVLLIV 15
                                                        ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL,
                                                                                                                                                                                                                                                      APPLICANT: McHenry, Charles S. Seville, Mark
Cull, Millard G.
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20004
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                                                                                                                                            STREET: 220 Montgome CITY: San Francisco
                                                                                                                               STATE: CA
                                                                                                             COUNTRY: USA
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419 Seventh Street, N.W.,
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VENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
VENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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b; Pred. No. 5.6
0; Mismatches
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; STRANDEDNESS: not relevant; TOPOLOGY: not relevant; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO US-08-928-213B-60
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Best Local :
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                                                                  TELEFAX: (206) 682-60: INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,11: FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                            SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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STRANDEDNESS:
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ATTORNEY/AGENT INFORMATION:
NAME: MSOFFICATION:
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98104-7092
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               amino acid
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TYPE: amino acid
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REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: ENZYCO-02550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/928,213B FILING DATE: 12-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Twardzik, Daniel R.
VERWION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
VERWION: AND DIAGNOSIS OF TUBERCULOSIS
EQUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campos-Neto, Antonio
Houghton, Raymond
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                                                                                                            (206)
                                                                                     682-6031
                                                                                                        622-4900
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                                                                      142:
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RESULT 26
US-09-056-556-142
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Sequence 142, Application US/09056556
                                                                                                                    Matches
                                                                                                                                Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/818
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                  267 amino acids
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VENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky, Yasir A.W. Dillon, Davin C.
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100.0%; Pr
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100.0%; F1
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                                                                                                                 s; Score 7; DB 4; Pred. No. 15; 0; Mismatches
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                                                                                                                                           Length 267;
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                                                                                                                                                                                                                                                                Sequence 9, Applic Patent No. 5928890
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                               236 QQTVAPQ 242
                                                                                                                                                     STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                       10 QQTVAPQ 16
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ZIP: 98104-7092
                                                                                                                                           STATE:
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CLASSIFICATION:
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; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-056-556-142
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS A
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARAE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,559B
FILING DATE: 06-JUN-1995
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                  COUNTRY: UNITED STATES OF AMERICA ZIP: 20005-3934
                                                                                                                                                                                                                                                  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
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100.0%; Pred. No.
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ATTORNEY/AGENT INFORMATION:

STEFFE, ERIC

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36,688

1488.0840000

REGISTRATION NUMBER:

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Query Match
Best Local Similarity
Thes 7; Conserve
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; MOLECULE TYPE: US-08-118-270-14
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                                                                                                                                                                                                    TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: not
MOLECULE TYPE:
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LENGTH: 365 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MUTELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                  TYPE: amino a STRANDEDNESS:
                                                                         TOPOLOGY:
                                                                                                                                                                        LENGTH:
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                                                                                                                                                                     377 amino acids
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MUTDBY, Randall B.
SCHUSTER, David I.
SCHUSTER, DAVID I.
VENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
VENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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100.0%; Pr
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Pred. No.
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Query Match

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Score 7;

DB 1;

Length 377;

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                          Sequence 31, Application PC/TUS9609848
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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TELEX: 248633
INFORMATION FOR SEQ ID NO:
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MEDIJIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: MUTELECOMMUNICATION INFORMATION: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                  Local Similarity
mes 7; Conserv
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                 ADDRESSEE:
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1700 Lincoln Street, Suite 3500
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MAY YORK University

VENTION: POLYPEPTIDES OF G-COUPLED PROTEIN

VENTION: RECEPTORS, AND COMPOSITIONS AND MI
                                                                                                                                                                                                                                                                               conservative (
                                                                                                                                                                                                                                                                                                                                                                                              linear
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9 Seventh Street, N.W.,
                Sheridan Ross & McIntosh
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                                                               PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
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                                                                                                                                                                                                                                                                                                   DB 5;
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PCT-US96-09848-15
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/486,036

FILING DATE: 07-JUN-1995

ATTORNEY/ACENT INFORMATION:

NAME: Connell, Gary J.

RECISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-33-PC:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
                              CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/486,036
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tripp, Cynthia ...
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                       SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 IVLLIVF 232
                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                    APPLICATION NUMBER: FILING DATE:
REFERENCE/DOCKET NUMBER:
            NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 IVLLIVE 11
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80203
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Denver
Colorado
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Colorado
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0; Mismatches
2618-33-PCT
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Query Match
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Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09086483A Patent No. 6214580 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (303) 863-02
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                               TELEFAX: (301) 309-84:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,483
                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 IVLLIVE 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: May-29-98 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/069,112 FILING DATE: Dec-9-97
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: May-30-97 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: HUMAN GENOME SCIENCES, STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 IVLLIVE 17
                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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 Similarity 7; Conserv
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3.0%; Score 7; 1
100.0%; Pred. No.
tive 0; Mismatc
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100.0%; Pred. No.
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                 DB 4;
                                  Length 467;
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Best Local Similarity
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US-09-013-895A-2
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US-08-390-000A-7
                                                                                                                                                                                                                 Sequence 2, Application US/09013895A
Patent No. 6342363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08390000A Patent No. 5985583
                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 7:
APPLICANT: Pan, James ...
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
TYPE: amino acid
TOPOLOGY: unvr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,000A
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                               APPLICANT: Ni, Jian APPLICANT: Rosen, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                225 LIVLLIV 231
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TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                             58 LIVLLIV 64
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1155 Avenue of the Americas
                                                                                                                                                Rosen, Craig A. Pan, James G.
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Cloning and Expression of
Gonadotropin-Releasing Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; F
tive 0;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 468
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US-08-194-338-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08194338 Patent No. 5474898
               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/676

FILING DATE: 28 MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: ISTAELSEN, Ned A.

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 371-26
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 27-JAN-19
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Venter, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 9410 KEY CITY: ROCKVILLE
                                                                                                                                           APPLICATION NUMBER: US/08/194,338 FILING DATE: 08-FEB-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                        STREET: 620 Newport
CITY: Newport Beach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                       COUNTRY:
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100.0%; Pred. No.
                                                                                                         US 07/676,174
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; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
US-08-087-772A-16
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US-08-087-772A-16
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Best Local Similarity
Watches 7; Conserve
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-194-338-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5691155
GENERAL INFORMATION:
                                   Matches
                                                                                                                                                                               TELEFAX: 919-00-10 1
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEQUENCE HARACTERISTICS:
1 PRIGTH: 477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339
                                                                                                                                                                                                                                            TELEPHONE: 919-881-3140
TELEPHONE: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS ADDRESSEE: Bell, Sel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
   225 LIVLLIV 231
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STRANDEDNESS: sir
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: NO. 5691155th Carolina
RY: USA
                                 Similarity 7; Conserv
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Post Office Drawer 34009
                                3.0%; Score 7; lilarity 100.0%; Pred. No. Conservative 0; Mismatc
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linear
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                                Mismatches
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                                                              Length 477
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                                 0,
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; ORGANISM: Streptomyces venezuelae US-09-320-878-2
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Best Local S
Matches 7
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APPLICANT: McGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 1835
TYPE: PRT
ORGANISM: Rattus sp.
                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 3739
TYPE: PRT
Query Match 3.0%; Score 7; DB 3; L
Best Local Similarity 100.0%; Pred. No. 1.9e+02
Matches 7; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mery C.
APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/100,880 EARLIER FILING DATE: 1998-09-22 EARLIER APPLICATION NUMBER: 60/087,080 EARLIER FILING DATE: 1998-05-28 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: CIP OF 09/141,908 EARLIER FILING DATE: 1998-08-28 EARLIER APPLICATION NUMBER: CIP OF 09/073,538 EARLIER FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/320,878A CURRENT FILING DATE: 1999-05-27
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100.0%; Pred. No. 98)
ive 0; Mismatches
                                           Length 3739;
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Indels

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APAAEET 470

150 APAAEET

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GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pil
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
RESULT 41
US-08-630-916A-89
US-08-630-916A-89
: Sequence 89, Application US/08630916A
; Patent No. 6011137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 33; LENGTH: 3739; TYPE: PRT; ORGANISM: Streptomyces venezuelae US-09-105-537-33
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                                                                                                                                                                                                                                                                             ORGANISM: Streptomyces venezuelae US-09-105-537-6
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
LENGTH: 11877
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/105,537A CURRENT FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43
                                                                                                                                      5413 APAAEET 5419
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nes 7; Conserv
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100.0%; Pr
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100.0%; Pred. No.
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0; Mismatches
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o. 5.9e+02;
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RESULT 42
US-08-630-915A-145
; Sequence 145, App
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Best Local Similarity
""" 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             Description US/08630915A Patent No. 6309820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 89:
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
NAME: MISROCK, S. LESLIE
                                           ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                             APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
APPLICANT: MCCONNELL, Stephen J.
APPLICANT: MCCONNELL, Stephen J.
APPLICANT: MCCONNELL, STEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FOwlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING NUMBER OF SEQUENCES: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1155 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 PGTPAP 151
                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                COUNTRY:
                                                                                                                                                       CITY: New York
                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
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                                                                                                RY: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: United States 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                   New York
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Fowlkes, Dana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
PatentIn Release #1.0, Version #1.30
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Pred. No.
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Best Local Similarity
6; Conserve
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US-08-792-832A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/08792832A Patent No. 6017734
                TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-8864/974:
TELEX: 66141 PENNIE
TRELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
                                              NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                           FILING DATE: 30-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,955
FILING DATE: 07-JUL-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/792,832A
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                       APPLICATION NUMBER: US 08 FILING DATE: 03-JUL-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Summers UI., Max. J.
APPLICANT: Braunagel Dr., Tao
APPLICANT: Hong Dr., Tao
APPLICANT: Hong Dr., Tao
UNIQUE NUCLEOTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFONMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 03-APR-19
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 PGTPAP 151
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.O. Box 4433
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N: 536
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SEQUENCE AND USES
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100.0%; Pred. No. 10;
tive 0; Mismatches
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                                                                                     TAMK: 190
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THEREOF
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US-08-792-832A-33
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                                                                                                 US-08-792-832A-33
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                                          Query Match
Best Local :
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Best Local :
                             Matches
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                                                                                                                                                                                    TELEFAX: 512/474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,832A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Summers Dr., Max D.
APPLICANT: Braunagel Dr., Sharon C.
APPLICANT: Hong Dr., Tao
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. B
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 IVLLIV 231
 226 IVLLIV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                          NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                TOPOLOGY:
                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60 FILING DATE: 07-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                          Local Similarity es 6; Conserv
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                                                                                                                                            ·amino acid
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P.O. Box 4433
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                                                                                                                                                        24 amino acids
                             Conservative
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                                      2.6%; Score 6;
100.0%; Pred. No.
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100.0%; Pred. No.
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                             Mismatches
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                                                     Length 24;
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                             Indels
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                            Gaps
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US-08-477-877B-56
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US-09-023-339-5
                                                                                                                                                                                                Sequence 56, Application US/08477877B Patent No. 5730979
                                                                                                                                                                                                                                                                                                                                                         Matches
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Atent No. 612/17.
Atent No. 612/17.
APPLICANT: Rutliff, Thomas D.
APPLICANT: Rodriguez, Raymond L.
APPLICANT: RODRIGUEZ, Raymond L.
APPLICANT: NO INVENTION: Production of '1-Antitrypsin in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Appr-
No. 612714
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bazin, Herv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/023,33
FILING DATE: 13-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,991
FILING DATE: 13-FEB-1997
ATTORNETY/AGENT INFORMATION:
NAME: PELLINOTY, JOANNE REGISTRATION NUMBER: P42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                          APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dominique
APPLICANT: Latinne, Dominique
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: RAMY1A
                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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STREET: Palo Alto
                                                                                                                                                                                                                                                                                                                          224 VLIVLL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                             11 VLIVLL 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
COUNTRY: UZIP: 07068
                                STATE:
                                                          STREET:
                                                                        ADDRESSEE:
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                                                                                          ADDRESSEE:
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                                                      6 Becker Farm Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 amino acids
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                        Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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BER: 0665-0003.30
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Mismatches
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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-477-877B-56
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/0:
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bazin, Herv
APPLICANT: Latinne, Dor
TITLE OF INVENTION: LO
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                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                   CLASSIFICATION:
                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                              STREET: 6 Becke
CITY: Roseland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/40 FILING DATE: 29-MAR-1995
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             APPLICATION NUMBER: 08/40 FILING DATE: 29-MAR-1995
                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                   6 Becker Farm Road
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                                                                                                                                                                 IBM PS/2
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                                 08/407,009
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Pred. No.
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; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-472-281A-56
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                                                                                         APPLICATION NUMBER: 08/407
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
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TITLE OF IN
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CURRENT APPLICATION NUMBER: US/08/477,989B
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MEDIUM TYPE: 3.5 inc
COMPUTER: IBM PS/2
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PRIOR APPLICATION DATA:
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                        NAME: Olstein, Elliot M. REGISTRATION NUMBER: 24,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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REFERENCE/DOCKET NUMBER: 61750-142
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EE: Cecchi, Stewart
6 Becker Farm Road
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Thereof for Inhibiting
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100.0%; Pred. No. 22;
ive 0; Mismatches
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Stewart & Olstein
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61750-147
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Watches 6; Conserve
                                                                                               US-08-792-832A-56
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GENERAL INFORMATION:
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                                                                                                                                                                                          TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                  FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/000,955 FILING DATE: 07-JUL-1995 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Summers Dr., Max D.
APPLICANT: Braunagel Dr., Sharon C.
APPLICANT: Hong Dr., Tao
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                                                                                                            STRANDEDNESS:
TOPOLOGY: 1i
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                            LENGTH:
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Conservative
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SEQUENCE AND USES
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b; Pred. No. 22;
0; Mismatches
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Conservative

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Mismatches

Indels

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Gaps

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2.6%; Score 6; I 100.0%; Pred. No.

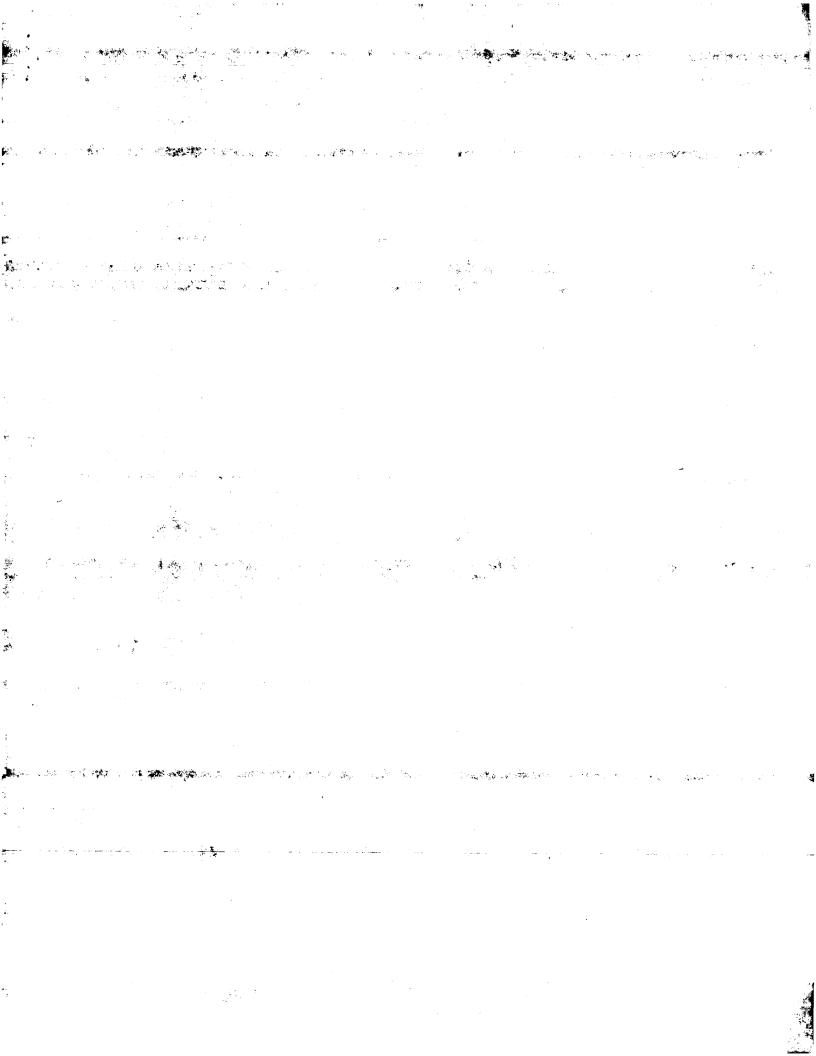
DB 3; ). 23;

Length 34;

0;

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION NO DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBBINS, ROBERTA L.
REFISTRATION NUMBER: 5150-0030
REFERNCE/DOCKET NUMBER: 5150-0030
REJECOMMUNICATION INFORMATION:
TELLEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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Search completed: August 13, 2002, 08:38:18 Job time: 192 sec
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                                                                                                                                                                            Query Match 2.6%; Score 6; DB Best Local Similarity 100.0%; Pred. No. 25 Matches 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
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                                                                  pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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AF012629 antagonist decoy receptor for TRAIL/Apo-2L (TRID)
mRNA complete cds.
AF012629.1 GI:2338430
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hominidae; Homo.

1 (bases 1 to 780)

Pan,G., Ni,J., Welly.F., Yu,G., Gentz,R. and Dixit,V.M.
An antagonist decoy receptor and a death domain-containing receptor
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                                                                                                                      for TRAIL (5327), 815-818 (1997) science 277 (5327), 815-818 (1997) 97390508
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AF013834 Homo sapi

AF03384 Homo sapi

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AF017885 Sequence

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AF017863 Homo sapi

AF01683 Homo sapi

AF016818 Homo sapi

AF017939 Homo sapi

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AF017959 Homo sapi
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FEATURES

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661 GCCCAGCTGCTGAAGAGACAATGACCAGCCAGCCGGGGGACTCCTGCCTCTTCTCATTAC
                                                                                                               661 gccccagctgctgaagagacaatgaccaccagcccggggactccttgcctctctcattac 720
                                                                                                                                                                                 601 agcccggggactcctgccccagctgctgaagagacaatgaccaccagcccggggactcct
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/ Product="antagonist decoy receptor for TRAIL/Apo-2L"
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/ Code: "AAB67110.1"
/ Code: "GI: 2338431"
/ Cranslation="MARIKTLKFVVVIVAVLLPVLAYSATTAROEEVPQOTVAPOQOETARSERIGACNPCTEGVDYIVASINIEPSCFPCTYCKSDOKHKSSCT MTROTYCOCKEGTERNENSPEMCRKCSRCPSGEVOYSNCTSMDDIGCVEEFGAMATVE TPADAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAETMNTSPGTPAPAAETMNTSPGTPAPAAETMNTSPGTPAPAAETMNTSPGTPAPAAETMNTSPGTPAPAAETMNTSPGTPAPAAETMNTSPGTPAPAAETMTSPGTPAPAAETMTSPGTPAPAAETMTSPGTPAPAAETMTSPGTPAPAAETMTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMTTSPGTPAPAAETMT
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Best Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MacFarlane, M., Ahmad, M., Srinivasula, S.M., Fernandes-Alnemri, T.,
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Identification and molecular cloning of two novel receptors for the 97467318

97467318
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Loases 1 to 900)

Ahmad M. Srinivasula, S.M., Fernandes-Alnemri, T.,
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//note="TNRR family member; binds cytotoxic ligand TRAIL; antagonistic decoy receptor, does not contain death
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/db_xref="taxon:9606"
/cell_type="7-lymphocyte"
/note="Jurkat"
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Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Gurney, A.L., Hillan, K.J., Marak, M.R., Marsters, S.A. Tumas, D., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment of imm diseases
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AX077019.1
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                                                                                   Patent:
       Similarity
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                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Patent WO0105972.
Score 777; DB 6;
Pred. No. 1.4e-210;
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A., Pitti,R
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                   Sheridan, J.P., Marsters, S.A., Pitti, R.M. Baldwin, D., Ramakrishnan, L., Gray, C.L., Goddard, A.D., Godowski, P. and Ashkenazi. Control of TRAIL-induced apoptosis by a decoy receptors Science 277 (5327), 818-821 (1997)
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GAGACAATGAACACCAGCCCAGGGACTCCTGCCCCAGCTGCTGAAGAGACAATGACCACC
                     gagacaatgaacaccagcccagggactcctgccccagctgctgcaagagacaatgaccacc
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
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Location/Qualifiers
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/p
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/db_xref="taxon:9606"
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193. .972
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                                                          ATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-JUL-1997) Biochemistry, Immunex, Street, Seattle, WA 98101, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1365)
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                                                                                                                                                                                                                                                                              /gene="TRAIL-R3"
/codon_start=1
/product="TMF related TRAIL receptor"
/protein_id="AGC05593.1"
/db_xref="G1:2957264"
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PKTLKEYVVIYAVLLEVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEH
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SPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMMTSPGTPAPA
AEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPA
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/db_xref="taxon:9606"
/chromosome="8"
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AF033854.1
                                                                 Mongkolsapaya, J., Cowper, A., Bell, J.I. and Screaton, G.R. Direct Submission
                                                                                                                        Mongkolsapaya,J., Cówper,A., Xu,X
Bell,J.I. and Screaton,G.R.
Lymphocytes inhibitor of TRAIL: A I
Lymphocytes from the death ligand
                                                                                                                                                                                                                                                                cds.
                              Submitted (10-NOV-1997) Immunology,
Medicine, John Radcliffe Hospital,
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                           McMichael, A.
                                                                                       McMichael, A.J.,
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                                               agcccggggactcctgccccagctgctgaagagacaatgaccaccagcccgggggactcct
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/function="TRAIL receptor"
/note="TNF receptor family
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Tumor necrosis factor receptor-associated protei
Patent: JP 2000078995-A 1 21-MAR-2000;
SMITHKLINE BEECHAM CORP
OS Unidentified
PN JP 2000078995-A/1
PD 21-MAR-2000
PF 01-SEP-1999 US 087/95910, 28-JUL-1997 US 087/95910, 28-JUL-1997 US PFEB-1997 US 08-7/95910, 28-JUL-1997 US PFTER R YOUNG, KONG B TAN, ANA RISA RENOX,
PI SALLY DOREEN PATRICIA LYN
PC C12N15/09, A61831/7052, A61838/00, A61845/00, A PC A61931/12,
PC A61931/12,
PC A61931/12,
PC A61931/10, A61937/02, C07K14/705, C07K16/28, C1
                                                                            aatgaaccttcttgcttcccatgtacagtttgtaaatcagatcaaaaacataaaagttcc
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R R YOUNG,KONG B TAN,ANA RISA RENOX,
SALLY DOREEN PATRICIA LYN
C12N15/09,A61K31/7052,A61K38/00,A61K45/00,A61K48/00,A61P31/04,
A61P31/12,
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/db_xref="taxon:32644"
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                                                                                                                                                                                                                                                                                                                                              Tschopp, J
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Schneider, P., Bodmer
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             MTRDTVCQCKEGTFRNVNSPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVE
TPAAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPG
TPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLVFV"
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/db_xref="G1:2529565"
/translation="MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQ
RHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCT
                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="liver and spleen"
/dev_stage="fetal"
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                                                                                                                                               /function="binds cytotoxic ligand TRAIL"
/note="DR4 homolog; contains no intracel
                                                                                                                                   /codon_start=1
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Sequence 2 :
AX088363
AX088363.1
                                     synthetic synthetic
artificial sequence.

1 (bases 1 to 1111)
Denome, S.A., Swain, P.M. and Tzellas,
A transmembrane trap for isolating m
Patent: WO 0114542-A 2 01-MAR-2001;
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Pred. No. 1.2e-209;
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/db_xref="taxon:35630"
/note="cDNA clone"
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1 (bases 1 to 947)

Denome, S.A., Swain, P.M. and Tzellas, N.
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/db_xxef="taxon:32630"
/note="cDNA clone"
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96.4%;
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Patent WO0114542.
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Pred. No. 8.7e-184;
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452; Conserv
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Eukaryota; M
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n,G., Ni,J. and Dixit,V.M.
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                                                                                                                                                                                                                                                                                                                                              /Product="TNF receptor-related receptor for TRAIL"
/Product="TNF receptor-related receptor-related receptor-rediction-"MGLMGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFI
/*CITALSTAILPRYDDSTIPRODEVPQOTVAPQOQRRSLKEEECPAGSFRWEIGSPGMKNPCTEG
VDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRATUTVCCEKGGDKNSPYKLLIIVV
GCPRGWYKVSNCTPRSDIKCKNBSAASSTGKTPAAEETVTTILGMLASPYHYLLIIVT
GCPRGWYKVSNCTPRSDIKCKNBSAASSTGKTPAAEETVTTILGMLASPYHYLLIIVT
LVIILAVVVVGFSCRKKFISVLKGICSGGGGPERVHRVLFRRSCPSRVPGAEDNAR
NUTISNRYLQPTQVSEQEIGGELAELTGVTVESPEEDPORLLEGAEAEGCQRRRLLVP
VNDADSADISTLDASATLEEGHAKETIQDQLVGSEKLFYEEDEAGSATSCL"
a 301 c 328 g 242 t
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receptor with a truncated death domain;
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/db_xref="taxon:9606"
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AF021232.1 GI:3452187
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Street, Se
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Smith, C.A. and Goodwin, R.G.
The novel receptor TRAIL-R4 induces NF-kappaB and
TRAIL-mediated apoptosis, yet retains an incomplet
Immunity 7 (6), 813-820 (1997)
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1 (bases 1 to 1588)
Degl1-Esposti,M.A., Dougall,W.C., Smolak,P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Seattle, WA 98101, USA
           Vtranslation="MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFI
VAVLLEVRVDSATIPRODEVPQQTVAPQQQRRSLKEEECPAGSHRSEYTGACURCTEG
VDYTLASNILPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKNSPEMCRTCRT
GCPRGWYKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASSYHYLLIIVV
LVIILAVVVVGFSCKKKFISYLKGICSGGGGPERVHRVLFRRSCPSRVPGAEDNAR
NETLSNRYLQPTQVSEQEIQELAELTGVTVESPEEPQRLLEQAEAEGCQRRLLVP
VNDADSADISTLLDAASATLEECHAKEFIQDQLVGSEKLFYEEDEAGSATSCL"

401 c 423 g 364 t
                                                                                                                                                                                                                             /note="New TRAIL
/allele="A"
79. .1239
                                                                                                                                /product="TRAIL-R4-A"
/protein_id="AAC32765,1"
/db_xref="GI:3452183"
                                                                                                                                                                              /gene="TRAIL-R4"
/note="New TRAIL
/codon_start=1
                                                                                                                                                                                                                                                                           /gene="TRAIL-R4"
                                                                                                                                                                                                                                                                                                                        /chromosome="8"
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/db_xref="taxon:9606"
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Homo sapiens decoy receptor 2
AF029761
AF029761.1 GI:4106963
         Ashkenazi,A.

Direct Submission
Submitted (14-OCT-1997) Molecular Oncology,
South San Francisco, CA 94080, USA
3 (bases 1 to 1726)
                                                                         Marsters, S.A., Sheridan, J.P., Pitti, R.M., Baldwin, D., Yuan, J., Gurney, A., Goddard, A.
                                                                                                                             A novel receptor for Apo2L/TRAIL contains Curr. Biol. 7 (12), 1003-1006 (1997)
                                                                                                                                                                            1 (bases 1 to 1726)
Marsters, S.A., Sheridan, J.P., Pitti, R.M.,
 Marsters, S.A.,
                                                                                                                 98044290
                                                                                                                                                    Ashkenazi, A.
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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82.0%;
  Sheridan, J.P.,
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Pred. No. 9.8e
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  Pitti, R.M.,
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Huang, A.,
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Godowski,P. and
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  Skubatch, M.,
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                                          cccagctgctgaagagacaatgaacaccagcccggggactcctgccccagctgctgaaga
                                                                                 TACGCCCCGGAGTGACATCAAGTGCAAAAATGAATCAGCTGCCAGTTCCACTGGGAAAAC
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452; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-JAN-1999) Molecular Oncology, South San Francisco, CA 94080, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Ashkenazi,A.
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VDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYEEDEAGSATSCL
432 C 443 9 411 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="inhibitory receptor for Apo2L/TRAIL"
/note="DCR2; member of the TNF receptor superfamily that
contains a truncated death domain"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-AUG-1997) Biochemistry, Street, Seattle, WA 98101, USA
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                                                                                                                                                                                                                                         Similarity
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mmalia; Eutheria; Primates; Catarrhini; Hominidae;
(bases 1 to 1333)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 1333)
                                                                                                                                                                                                                                                                                                                   333
                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /allele="B"
                                                                                                                                                                                                                                                                                                                              'translation="MGLWGOSVPTASSARAGRYPGARTASGTRPWILDSKILKEVVFI
VAVILLEVRVDSATIPRODEVPGOTVAPOQORRSIKEEECPAGSHRSEYIGACNECTEG
VDYTLASNNILESCLLCTVCKSGOTNKSSCTTFRDTVCOCEKGSFODKKSPEMCRTCRT
GCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILGMLASPYHYLIIIVV
LVIILAVVVVGFSCRKKFISYLKGICSGGGGFERVHRVLFRRSCPSRVPGAEDNAR
NETLSNRYLGPTQVSEBGEIGGGELAELTGVTVELPEBPGALEOAEAECGRRALLVP
VNDADSADISTLLDASATLEEGHAKETIQDQLVGSEKLFYEEDEAGSATSCL"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC32766.1"
/db_xref="GI:3452185"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="TRAIL-R4-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="New TRAIL receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="8p22-p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="TRAIL-R4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                         Score 379.8; DB 9
Pred. No. 2.7e-97;
0; Mismatches 97
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(TRAIL-R4)
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mRNA,
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REMARK
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                                                                                    Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.lln Series: IRAK Plate: 21 Row: b Column: 21 This clone was selected for full length sequencing because passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens, superfamily, n
                                                                                                                                                                                                                                  Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., F
A.M., Holloway, M., Telford, B, Hodgson,
                                                                                                                                                                                                                                                                                                            Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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nmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 1723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:9365 IMAGE:3
                                                      Location/Qualifiers
1. .1723
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IMAGE:3857315, mRNA,
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              tacgtcctgggatgatatccagtgtgttgaagaatttggtgccaatg 469
                                                                                                                                         catgaccagagacacagtgtgtcagtgtaaaggaaggcaccttccggaatgaaaactcccc
                                                                                                                                                                                                                 accttcttgcttcccatgtacagtttgtaaatcagatcaaaaacataaaagttcctgcac
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TACGCCCTGGAGTGACATCGAGTGTGTCCACAAAGAATCAGGCAATG
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/protein_id="AAH12866.1"

/db_xref="G1:15277527"

/db_xref="G1:15277527"

/translation="MARPPARVHLGAFLAVTPNPGSAASGTEAAAATPSKVWGSSAGR

IEPRGGGRGALPTSMGOHGPSARARAGRAPGPRPAREASPRLRVHKTFKFVVVGVLLQ

VVPSSAATIKLHDQSIGTQQWEHSPLGELCPPGSHRSEHEPACNRCTEGVGYTNASNN

LFACLPCTACKSDEEERSPCTTTRNTAGOCKPGTFRNDNSAEMCRKCSRGCPRGMVKV

KDCTFWSDIECVHKESGNGHNLWVILVVTLVVPLLLVAVLIVCCTIGSGCGGDPKCMD

RVCFWRLGLLRGPGAEDNAHNEILSNADSLSTEYSEQQMESQEPADLTGVTVQSPGEA

QCLLGPAEAEGSQRRRLLVPANGADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKN

EIDVVRAGTAGPGDALYAMLMKWVNKTGRNASIHTLLDALERMEERHAKEKIQDLLVD

SGKFIYLEDGTGSAVSLE"

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/note="Vector: pC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Ovary, adenocarcinoma"
/clone_lib="NIH_MGC_66"
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Pred. No. 6e-55;
0; Mismatches 106;
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Search completed: August 13, Job time: 8613 sec 2002, 11:21:04

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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CC An antibody against the TRAIL receptor TRAIL-R3 of the invention.
CC An antibody against the TRAIL receptors is useful for detecting mammalian.
CC DAS or TRAIL-R3 proteins in a sample. Recombinant cells are useful in
CC bloassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.
CC (Ant)agonists identified by the assay are useful for modulating the
CC related conditions which are treated in this way, include cancer
CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus
CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders
CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral
CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial
CC infarction and stroke). The polynucleotides can also be used to treat
CC used to form a composition that is useful for inhibiting expression of a

NXX
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A, Godowski PJ, Gurney,
Tumas D, Watanabe CK, W
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                                                                Wood WI,
                                                                        Filvaroff E,
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AAS21244-AAS21518 encode for novel human secretory and transmembrane CPRO polypeptides. The PRO polypeptides are useful to detect other CPRO polypeptides, to link bioactive molecules to cells expressing CPRO polypeptides, to modulate biological activities of cells expressing CPRO polypeptides, and to detect the presence of mammalian lung, colon, CD breast, prostate, rectal, cervical or liver tumours by comparing PRO CPRO polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the CR proliferation or differentiation of chondrocytes, the proliferation or GC cartilage, the proliferation of inner ear utricular supporting cells or CC of T-lymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC to factor VIIA. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The polynucleotides encoding CC PRO polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.
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No. 4.3e-224;
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also designated Apo-2DcR. The clone was obtained from a yeast screening of human breast carcinoma library cDNA. Apo-2DcR (27 kDa, pI 4.84) shows homology to apoptosis-linked receptors of the tumour necrosis factor receptor family, such as DR4 and Apo-2. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO366. Claimed compositions comprising these proteins or their agonists are useful for increasing comprising these proteins or their agonists are useful for increasing

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                                                                                                                                                                                                                                                                                                             New PRO polypeptides, nucleic acids and (ant)agonists, diagnosing and treating immune-related disorders, such sclerosis, rheumatoid arthritis and diabetes -
                                                                                                                                                                                          The present novel human
                                                                                                                                                                                                                                                                     Claim 21;
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P-PSDB; AAB20111.
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                                                                                                                                                                                                                                                                Fig 7; 127pp;
                                                                                                                                                                                          sequence is that of cDNA clone DNA33085-1110 encoding immunomodulator protein PRO366 (UNQ321) (see AAB20111),
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Tumas D, Watanabe CK;
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cc autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinated diseases (such as multiple sclerosis), autoimmune chronic active hepatitis, primary cc multiple sclerosis, granulomatous hepatitis, sclerosing cholangitis, cc inflammatory bowel disease (ulcerative colitis and Crohn's disease), cc quiten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated cc skin diseases (such as bullous skin diseases, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, catopic dermatitis, food hypersensitivity and urticaria), immunologic cdiseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed). Cc atopic dermation of diagnosing these disorders comprise detecting ct the level of expression of the PRO gene. Also claimed are a method cof identifying a compound capable of inhibiting the expression or cactivity of the PRO polypeptide, vectors, host cells, antibodies and a method of stimulating an immune response by administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          increasing the proliferation of T-lymphocytes in a mammal in respons to an antigen. Claimed compositions comprising the PRO polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering the PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
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New isolated nucleic acid genetic disorders and trea

disorders and nic disorders,

treating such as a

for producing a PRO polypeptide, ating cardiovascular, endothelial has atherosclerosis, wounds or ca

2001-090793/10. DB; AAB53091.

Claim 58;

Fig

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15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
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                                                                                                                                                                                                                      26-JUL-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                Homo
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                                                                                                                                                             30-NOV-1999;
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14-MAY-1999;
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99WO-US21090.
99WO-US21547.
99WO-US23089.
99WO-US28313.
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CC protein, PRO antibodies specific for a PRO protein, fusion proteins CC comprising a PRO protein, agonists or antagonists of a PRO protein, and CC compounds which inhibit the expression of a PRO gene. The invention CC additionally encompasses methods of identifying modulators of PRO CC angiogenic disorder, or a susceptibility to such a disorder by detecting CC angiogenic disorder, or a susceptibility to such a disorder by detecting CC angiogenic disorder, or a susceptibility to such a disorder by detecting CC angiogenist or antagonist; a retroviral gene therapy vector comprising a CC PRO nucleic acid; and methods of inhibiting or stimulating enothalial or angiogenist cell growth, cardiac hypertrophy or PRO induced angiogeness via the administration of a PRO protein, pro nucleic acids, pro proteins, antibodies against pro proteins, it cardiavascular, endothelial or angiogenist or antagonist therapeof. CC aponists and PRO antagonists may be used as therapeutic agents to treat CC cardiovascular, endothelial or angiogenic disorders, such as thereosclerosis, osteoporosis, myocardial infarction, hypertension, CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, C disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to soraer libraries to isolate cDNAs with sequence identity to PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic content of the development and screening of potential contents. The present sequence represents a cDNA encoding a PRO protein of the invention.
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cDNA clone DNA33085 codes for human Apo-2DcR (see AAW88408), a member of the tumour necrosis factor receptor family that binds Apo-2 ligand. It was isolated by: transformation of yeast with

novel

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RESULT
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P-PSDB; AAW84347.
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                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                 Human Apo-2DcR cDNA clone DNA33085
                             Claim 36; Page 51-53;
                                            New Apo-2DcR polypeptide
apoptosis, e.g. in neurod
                                                                                                   Ashkenazi AJ,
                                                                                                                                                                                 WO9858062-A1
                                                                                                                                                                                                                                                                                                                  therapy;
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                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                   18-JUN-1997;
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CC vector incorporating human breast carcinoma cDNA; isolation of CC yeast clones secreting amylase; PCR amplification (see AAV8419-50) CC of the insert directly from the yeast colony and purification of CC DNA for sequencing; use of an isolated sequence (DNA21705) as a CC probe to screen a human foetal lung library; and isolation of the CC full-length clone, which is deposited as ATCC 209087. An CC alternative translational initiation site encodes amino acid CC residues -40 to 259 of Apo-2DcR (see AAW88409). The invention CC provides vectors and host cells for recombinant production of CC apo-2DcR polypeptides, antibodies, and transgenic and knockout CC animals (useful e.g. for screening and developing drugs that protect CC against excessive apoptosis). Apo-2DcR, or chimeras comprising CC Apo-2DcR or its extracellular domain fused to a heterologous C claimed) and/or NF-KappaB activation by Apo-2 ligand, and may be C claimed) and/or NF-KappaB activation by Apo-2 ligand, and may be used in wivo or ex vivo for gene therapy. They can be used in CC methods for the modulation and diagnosis of apoptosis e.g. in cases of neurodegeneration, autoimmune diseases and inflammation. Most thuman tumour cells do not express Apo-2DcR transcripts, but normal C cancer cells by Apo-2 ligand, possibly by protecting normal, but concerned the cancerous, cells.
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                                                                                          The present sequence encodes human tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be used for inhibiting the biological activities of TRAIL or for purifying TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated disorder such as T cell death in HIV-infected patients. They can be used for treating thrombotic dicroangiopathies such as thrombotic thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic acids can also be used for gene therapy. They can also be used carriers for delivering attached agents to cells bearing TRAIL.
                                                                                                                                                                                                                                                          New isolated TRAIL binding protein - which binds to a tunecrosis factor-related apoptosis inducing ligand, used diagnosis and treatment of TRAIL-mediated disorders
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RESULT ANUSCEP PT S19.
FT S19.
c receptor, TRS (see AAW76331). An expressed sequence tag (EST 213397) to derived from a cDNA libray made from human prostate was found to have sequence similarity to the human tumour necrosis factor (TNF) creceptor. A search through several overlapping ESTs indicated that this represented the 5' most EST of the assemble and so it was completely sequenced. Analysis of the 1410 cDNA sequence indicated that it encoded a complete open reading frame for a novel member of the TNF receptor superfamily. A polynucleotide encoding TRS can be obtained from a cDNA library derived from mRNA in cells of prostate, endothelial cells, interleukin-1 beta-treated smooth muscle cells, foetal liver spleen cells, and pregnant uterus using enapresed sequence tag analysis. Treatment of a subject in need of cenhanced TRS polypeptide activity comprises administering an agonist to the polypeptide and/or providing TRS polynucleotide in a form so cc as to effect production of the polypeptide activity in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stroke; ischaemia; acute respiratory disease syndrome; psoriasis; restenosis; brain injury; AIDS; bone disease; cancer; atherosclerosis; Alzheimer's disease; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury, AIDS and bone diseases
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RESULT AND STATE OF S
  CC AAZ2103 to AAZ21102 encode new human secreted proteins and AAY29861 to CX sequences. AAZ21103 to AAZ21112 represent probes for the secreted CX proteins. The polynucleotides and proteins are predicted to have CX biological activities which would make them suitable for treating, CX preventing or ameliorating medical conditions in humans and animals, CX although no supporting data is given. Suggested activities include cX activity, immune stimulating (e.g. as vaccines) or suppressing activity, that is given activity, hammone stimulating (e.g. as vaccines) or suppressing activity, activity, indicativity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory cx and thrombolytic activity, receptor/ligand activity, anti-inflammatory cx inhibition activity. The polynucleotides and proteins can also be used cx surce and use as a source or supplements. Such uses include use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen cx source and use as a source of carbohydrate. They may also have utility in compositions used for bone, cartilage, tendon, ligament, and/or nerve cx issue growth or regeneration, as well as for wound healing and tissue crepair and replacement, and in the treatment of burns, incisions and cx it the healing of bone fractures and cartilage damage or defects in humans cx and other animals.
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and other anim
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14-MAY-1998;
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Tumour necrosis factor receptor;
developmental abnormality; gesta

eptor; signal transducer molecule; gestational abnormalitity: prostat

prostate

TNF; cancer;

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CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active control in active fragments, and isolated TNF related ligands 1 and 3 (TNRI1 and TNRI3) or their active fragments. APO4 is useful for diagnosing prostate cancer context determining levels of APO4 is useful for diagnosing prostate cancer context. APO4 polypeptides are also useful for identifying selective be treated using APO4 selective binding agents linked to a therapeutic context. APO4 polypeptides are also useful for identifying selective context. APO4 polypeptides are also useful for identifying selective context. APO4 polypeptides are also useful for identifying selective context. APO4 polypeptides are also useful for identifying selective context. APO4 polypeptides are also useful for sextracellular, or context. APO4 polypeptides, active fragment which is extracellular, or context. APO4 polypeptides, active fragments are also useful for screening context. APO4 polypeptides, active fragments useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active context. APO4 polypeptides are also identified using APO4 polypeptides/active with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vitro. APO9 polypeptides are also identified using APO4 is also useful for diagnosis/treatment of developmental or gestational also context. APO6 was transfected to human breast carcinoma cell line approaches.
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Best Local
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                                            gaacatactggagcctgtaacccgtgcacagagggtgtggattacacccaacgcttccaac
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The present invention relates to methods for identifying a transdomain (TM) of a membrane-spanning protein. The method comprises modifying a nucleic acid encoding a death domain (DD)-lacking me spanning protein (e.g. Trail Receptor without Intracellular Doma by replacing the nucleic acid encoding the TM of the DD-lacking

comprises

Domain; membrane

TRID)

transmembrane

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                                                                                                                                                                                                     Identifying a transmembrane domain of a membrane-spanning protein useful in defining processes in cell suicide and tissue homeostasis, comprises modifying the nucleic acid encoding a death domain-lacking membrane spanning protein
                                                                                                                                                            Disclosure;
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cc which expresses a DD-containing receptor. The absence of apoptosis of the CC host cell is determined following exposure of the transfected cell to an CC apoptosis inducing ligand. Candidate nucleic acids encoding TM prevent CC apoptosis of the host cell. The modified nucleic acid encoding the CC modified death domain-lacking membrane-spanning protein can also include CC a nucleic acid sequence encoding an epitope tag. The present sequence is CC the coding sequence for a FLAG-TRID clone, which was used in the method CC of the present invention. This sequence comprises the human TRID coding CC sequence and a sequence encoding the FLAG-epitope tag. The FLAG-epitope CL is a useful marker to purify proteins encoded by the modified DD-lacking CC membrane-spanning protein. The identified TM and membrane-spanning CC proteins may be used in defining processes involved in cell suicide and CL issue homeostasis, and to evaluate, interfere and treat events, such as CC cell proliferation and cell-cell signalling pathways.
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The present invention relates to methods for identifying a transmembrane domain (TM) of a membrane-spanning protein. The method comprises modifying a nucleic acid encoding a death domain (DD)-lacking membrane spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID by replacing the nucleic acid encoding the TM of the DD-lacking membrane-spanning protein with a candidate nucleic acid sequence to produce a nucleic acid encoding a modified DD-lacking membrane spanning protein. The modified nucleic acid is then transfected into a host cell, which expresses a DD-containing receptor. The absence of apoptosis of the host cell is determined following exposure of the transfected cell to an apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent apoptosis of the host cell. The modified nucleic acid encoding the modified death domain-lacking membrane-spanning protein can also include
                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a transmembrane domain of a membrane-spanning protein useful in defining processes in cell suicide and tissue homeostasis, comprises modifying the nucleic acid encoding a death domain-lacking
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                                      ccagctgctgaagagacaatgaccaccagcccggggactcctgcccagctgctgaagag
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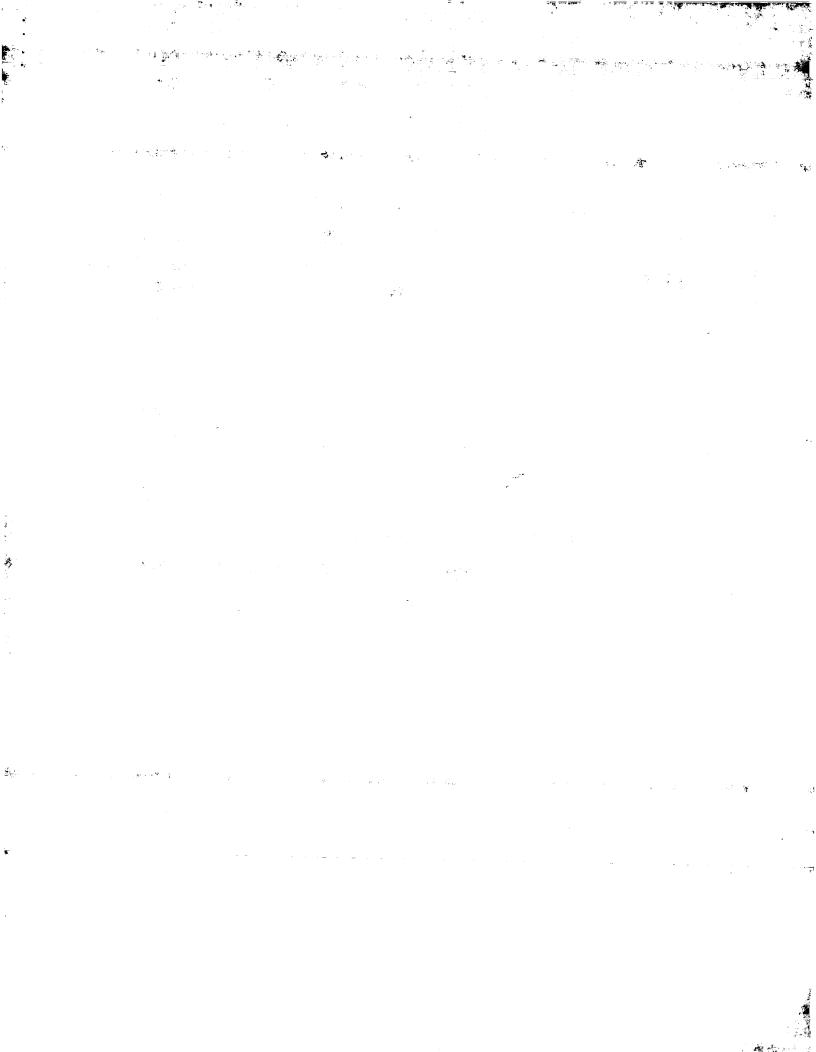
acaatgaccaccagcccggggactcctgccccagctgctgaagagacaatgaccaccagc

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Query Match
Best Local Similarity
Matches 452; Conser
                                                                                                                The present sequence is a cDNA encoding human receptor-associated protein (HRAP) from Incyte clone 3472455 obtained from LUNGNOT27 cDNA library. This sequence is expressed in musculoskeletal, cardiovascular and urologic tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiarthritic, antifheumatic, osteopathic, antiallergic, antianemic, antiasthmatic, antidiabetic, dermatological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and
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Search completed: August 13, 2002, 11:24:56 Job time: 8595 sec

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Listing first 45 summaries
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                US-07-814-220-3

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Sequence 2, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 65, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli

ALIGNMENTS

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Sequence 1,
Patent No. 6
                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF34
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                               TELEPHONE: (301) 309-851
TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
                                FEATURE:
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                                                                                                                                                 MOLECULE TYPE:
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TYPE: n
NAME/KEY:
LOCATION:
                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                              LOCATION:
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                                                                                    Sequence 1, Application Patent No. 6214580 GENERAL INFORMATION:
                                                                APPLICANT: NI, et al. TITLE OF INVENTION: H
                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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US-09-086-483A-1
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NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENCTH: 3566 base pairs
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 452; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,48
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COMPUTER READABLE
MEDIUM TYPE: F1
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NAME/KEY:
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LOCATION:
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                                                                                                                                                                                            66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/050,936 FILING DATE: May-30-97
                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                CACGACCAGAGACACCGTGTGTCAGTGTGAAAAAGGAAGCTTCCAGGATAAAAACTCCCC
            TACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTT
                                           Conservative
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109..1266
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274..1266
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82.0%;
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                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUIENCE CHARACTERISTICS:
LENGTH: 398 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                     Query Match
Best Local Sim
Matches 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09086483A Patent No. 6214580 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0
FILING DATE: May-29-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: May-30-97
                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8439
TELEFEX: (301) 309-8439
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HU NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                TOPOLOGY: 11
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PRIOR APPLICATION DATA:
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FILING DATE: Dec-9-97
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CCTTATCATCA
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                                                    Conservative
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                                                 Score 262.8; DB 4;
Pred. No. 2.5e-71;
0; Mismatches 2;
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                                                                            Length
                                                    Indels
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1407)
; OTHER INFORMATION: Human TRAIL Receptor Coding US-09-505-250-2
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US-09-505-250-2
Sequence 2, Application US/09505250A
Patent No. 6329148
Patent No. 6329148
GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
APPLICANT: Kao, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TITLE OF INVENTION: Triptclides and Death Domain Ligands
FILE REFERENCE: SUN-109RV2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/505,250A CURRENT FILING DATE: 2000-02-15 NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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TYPE: DNA
ORGANISM: H. sapiens
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agagatgtgccggaagtgtagca---
                                                               catgaccagagacacagtgtgtcagtgtaaagaaggcaccttccggaatgaaaactcccc 365
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                                            cacgaccaggaacacagcatgtcagtgcaaaccaggaactttccggaatgacaattctgc
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73.2%;
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; NAME/KEY:
; LOCATION:
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Best Local Similarity
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K,
REGISTRATION NUMBER: 36,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
FORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/09/013,895A FILING DATE: 27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                               126
                                                              330
                                                                                                                           276 CCGGGTCCACAAGACCTTCAAGTTTGTCG-----TCGTCGGGGTCCTGCTGCAGGTCGT 329
381
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: lin
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ZIP: 20850
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                                                                                    agcttactctgccaccactgcccggcaggaggtagttccccagcagacagtggccccaca 125
             gcaacagaggcacagcttcaaggggggggggtgtccagcaggatctcatagatcagaaca 185
                                                              ACCTAGCTCAGCTGCAACCATC
GCAATGGGAACATAGCCCTTTGGGAGAGTTGTGTCCACCAGGATCTCATAGATCAGAACG 440
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Pan, James G.
Gentz, Reiner L.
Dixit, Vishva M.
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9410 KEY WEST AVENUE
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                                                                                                                                                                                        Score 229.8; DB 4;
Pred. No. 7.6e-61;
0; Mismatches 107;
                                                                                                                                                                                                                        Length 2152;
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                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 26-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UMABER: US-
FILING DATE: 04-JUN-1997
                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1323 base pair
                                                                                                                                                                                                                             FILING DATE: US 08/815,255
PRIOR APPLICATION UMBER: US 08/700 oct
PRIOR DATA:
APPLICATION UMBER: US 08/700 oct
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
PRIOR DATE: 28-MAR-1997
                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                     FILING DATE: 28-MAR-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rauch, Charles
APPLICANT: Walczak, Henning
TITLE OF INVENTION: Receptor That Binds TRAIL
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                           TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                 TELLEFAX: (4. 756822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       621 TGAGATGTGCCGGAAGTGCAGCACAGGGTGCCCCAGAGGGATGGTCAAGGTCAAGGATTG
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OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version 6.0.1
                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                           FILING DATE:
             STRANDEDNESS:
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                                                                                                            (206) 233-0644
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linear
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             single
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BER: 32,172
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FEATURE:

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US-08-883-036A-1
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SEQ ID NO
LENGTH:
                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local
                         APPLICANT: Ashkenazi, Avi J.
APPLICANT: Ashkenazi, Anan
APPLICANT: Kim, K. Jin
APPLICANT: Kim, K. Jin
APPLICANT: Kim, K. Jin
APPLICANT: Kim, K. Jin
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE
FILE REFERENCE: P1468R1 (REVISE)
CURRENT APPLICATION NUMBER: US/09/329,633A
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/089,253
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 2
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Pred. No. 7.6e
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RESULT 8
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Best Local
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                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                                                  STREET: 1 DNA Way
CITY: South San F
STATE: California
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                                                                                                                     COUNTRY:
APPLICATION NUMBER: FILING DATE:
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               US/09/079,029
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Pred. No. 3.4e-50;
0; Mismatches 180;
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ATTORNEY/AGENT INFORMATION:

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APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RETITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION UMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
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                                                                                                                                                                                 Sequence 1, Application US/09333593A Patent No. 6313269 GENERAL INFORMATION:
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Best Local Similarity
Matches 316; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 1799 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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REGISTION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
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                                                                   RELATED RECEPTOR
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; LOCATION: (3538)(3598)(3601)(3607)(3608)(3619)(3632)(3659)(3686)(3690)
US-09-333-93A-1
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; SEQ ID NO 1
; LENGTH: 3881
TYPE: DNA
; ORGANISM: HOMO SAPIENS
                                                                                                                                                            Sequence 15, Application US/09006353A Patent No. 6261801
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Best Local Similarity
Matches 323; Conserv
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PRIOR FILING DATE: 1997-C
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Win
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PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1997-05-09
                                                                                                                                                GENERAL INFORMATION:
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                                          APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS
NUMBER OF SEQUENCES: 26
                                                                                                              APPLICANT:
APPLICANT:
                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             540
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               ADDRESSEE:
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YU, GUO-LIANG
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HUMAN GENOME
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 AVENUE
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               SCIENCES,
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Pred. No. 4.9e-50;
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                                                                                                                                                                                  GENERAL INFO
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                            Sequence 3, Application US/09333593A Patent No. 6313269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                  APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONE B.
APPLICANT: TRUNCH, ALCE B.
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BROOKES, ANDERS A REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ccacagcaacagaggcacagcttcaaggggga--ggagtgtccaggcaggatctcatagat 178
                                                                                                                                                                                                                                                                                                                                                                         432 ANATGNA--CTTTTTNGTTCCCTGTTANATTTTTAATT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 GTCCTAGCTTACTCTGCCACCACTGCCCGGCA-GAGGAAGTTNCCCAGCAGNCANTGGNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 gtcctagcttactctgccaccactgcccggcaggaaggttcccccagcagacagtggcc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cagaacatactggagcctgtaacccgtgcacagagggtgtggattacacccaacgcttcca 238
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                                                                                                                                                                                  YOUNG, PETER R.
MARSHALL, LISA A.
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                                                                                                                                                                                                                      DEEN, KEITH C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            506 base pairs
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81.7%;
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Pred. No. 2.6e-41;
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RESULT 12
US-09-006-353A-17
; Sequence 17, Application US/09006353A
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SEQ ID NO 3
LENGTH: 1062
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Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6261801
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 08/PRIOR FILING DATE: 1997-05-09
INFORMATION FOR SEQ
                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GENTZ, REINER APPLICANT: RUBEN, STEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 ccagctgctgaag 496
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                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                        APPLICATION NUMBER: US/09/006,353A FILING DATE:
                                                                                                                                                                                                                                                                                                   COUNTRY: U:
ZIP: 20850
                                                                                    REGISTRATION NUMBER: 36,373
                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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9410 KEY WEST AVENUE
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                  (301)
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ID NO:
                  309-8512
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67.2%;
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US-09-006-353A-18
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                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 base pairs
TYPE: nucleic acid
                                             Query Match
Best Local Similarity 91.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
NAME: BROOKES, ANDERS 36,373
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435
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APPLICANT: 1
APPLICANT: 1
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LENGTH: 340 base pairs
TYPE: nucleic acid
                              649
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                GCCCCAGCTGCTGAAGAGACAATAATCACCAGCCCGGGGACTCCTGNNTCTNCTNATTAC 67
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9410 KEY WEST AVENUE
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RUBEN, STEVEN
VENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEI, YING-FEI
YU, GUO-LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                              DNA (genomic)
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91.3%;
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                                                                                                                                                                                                                                                                                             PF341
                                                        Score 91.6; DB 4;
Pred. No. 7e-19;
0; Mismatches 9;
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Pred. No. 1e-19;
0; Mismatches 9;
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                                                         9;
                                                                                     Length 241;
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US-09-006-353A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.1%;
Best Local Similarity 48.8%;
Matches 106; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFFLACE.
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
NAME: BROOKES, ANDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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CORRESPONDENCE ADDRESS:
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602 gcccggggactcctgccccagctgctgaagagacaatgaccaccagcccgggggactccttg 661
                                                                                                                                                                               542
                                                                                                                                                                                                                                                   880 CCCGGGCTGGTGGTCATTGTCTCTTCAGCAGCTGGGGCAGGAGTCCCCGGGCTGGTGGTC 821
                                                                                                                                                                                                                                                                                       482 ccccagctgctgaagagacaatgaacaccagcccggggactcctgccccagctgctgaag 541
                                                                                                           820 ATTGTCTCTTCAGCAGCTGGGGCAGGAGTCCCCGGGCTGGTGGTCATTGTCTCTTCAGCA 761
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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261..959
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Pred. No. 0.018
0; Mismatches
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0.018;
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US-07-814-220-3
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US-07-814-220-3
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Patent No. 5925
                                                                                                                                                                                                                           Query Match 5.0%;
Best Local Similarity 50.5%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437

FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/814,220
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Szumanski, Maria B.W.

APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
                                                                                                               586
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                 646 agcccggggactcctgccccagctgctgaagagacaatgaccaccaccagcccggggactcct 705
                                                                                                                                                                         526 gccccagctgctgaagagacaatgaacaccagcccagggactcctgccccagctgctgaa 585
169
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                               gagacaatgaccaccagcccggggactcctgccccagctgctgaagagacaatgaccacc 645
                                                                       GCGACCGCAGCAGCGGCGGCAGCTACTGCGGCGACCGCAGCAGCGGCTGCGGCAGCT 168
                                                                                                                                                 GCCGCGGCAGCAGCAGCTGCTACTGCGGCGACCGCAGCAGCGGCTGCGGCAGCTACTGCG 108
ACCGCTGCTACCGCAGCAGCTGCTGCGGCAGCAACTGCGGCGACCGCAGCAGCAGCGGCTGCG 228
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Pred. No. 0.01;
0; Mismatches 93;
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Qy 706 gcctcttc 713
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Db 229 GCAGCTAC 236
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Search completed: August 13, 2002, 11:26:06 Job time: 6722 sec

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Title:
Perfect score:
Sequence:
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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    GenCore version 4.5 (c) 1993 - 2000 Comp
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    2002122222
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AAW64668
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AAB53091
AAW296331
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AAY2964
AAY00933
AAW94671
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Tumour necrosis fa
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                                                                                     n TRID protein
Apo-2DcR pro
PRO366 polyp
n immunostimul
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.5 27.7 4	27.7 41	.5 28.8 42	48 32.4 4	32.4 4	32.7 4	32.7	32.7	34.2	34.2	34.2	472 34.2 468	34.2	34.2	34.2	34.2	34.2	34.2	45.4	45.4	45.9	45.9	45.9	45.9	34 45.9	45.9	34 45.9	34 45.9	1.5 92.7	67.5 99.0	375 99.5	376 99.6	.382 100.0	100.0
20	20	22	19	19	21	20	20	22	21	21	21	21	20	20	19	22	20	20	20	22	22	22	21	21	20	20	20	22	22	20	20	21	0
ω	AAW93576	AAB48352	AAW79260	AAB99284	AAB01340	AAY05725	AAY00934	AAB49241	AAB01339	AAB08546	AAY72023	AAY72022	AAW93609	AAY31602	AAW64483	AAB50896	AAW93577	AAW99019	AAY04144	AAB50892	AAB31187	AAU12341	AAY69991	AAB01341	AAW92792	AAW99018	AAW98200	AAB82182	AAB82181	AAY05726	AAW93578	AAB01343	AAWOO4U9
Human DR5 protein	hAPO8 prote	H	0		ated apop	Tumour necrosis fa	Human DR5s protein	DR4 p		Amino acid sequenc	Human Death Domain	Deat		Human death recept	Human DR4 protein.	DR4.	APORP		Human Tango-74 pro	TR10	acid se		n recept	elate	TNF re	n TRAIL re	bitor o	clone	RID clone	r necrosis f	Human hAPO9 protei	ptor.	nullan Apo-zock pro

## ALIGNMENTS

RESULT AAW64668

 $\vdash$ 

AAW64668 standard; Protein;

259

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Human TRID protein

AAW64668; 23-OCT-1998

(first entry)

TRAIL receptor without intracellular domain; TRID; TNFR-5; human; tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand; haematopoietic tissue; immune system; ligand; apoptosis; treatment.

ЪТ	FT.	ΗT	FT	FT	FΤ	FT	FT	FT	FΤ	FT	FT	FΤ	FT	FT	FT	FΤ	FH	XX	SO
Region		Region		Protein		Peptide			Homo sapiens.										
126136	/label= epitope	110122	/label= epitope	91102	/label= epitope	7985	/label= epitope	6876	/label= epitope	5866	/label= epitope	4252	/label- TRID	27259	/label= signal	127	Location/Qualifiers		

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RESULT
AAWB8408
ID AAW8
XX
AC AAW8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     TRID is a member of the tumour necrosis factor receptor (TNFR) family also known as TNFR-5. TRID is expressed in haematopoietic tissues and other normal human tissues. For a number of immune system-related disorders, substantially altered (whether increased or decreased) levels of TRID gene expression can be detected, therefore the TRID polypeptides, nucleic acids and antibodies are useful in the diagnosis of such immune system related disorders. Mutations of the TRID gene can also be used to identify ligands which may be useful in the treatment of apoptosis related disorders. TRID is administered to humans at a parenteral dose of 0.01 to 1 mg/kg/day.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a human TRID (TRAIL apoptosis-inducing ligand) receptor without a TRID is a member of the tumour necrosis factor also known as TNFR-5. TRID is expressed in ha
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Yu G;
            AAW88408;
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                                    AAW88408
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DB; AAV51348.
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                                                                                                                                                                                                      SPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAE 180
                                                                                                                                           etmntspgtpapaaeetmttspgtpapaaeetmttspgtpapaaeetmttspgtpasshy
                                                                                                                                                                    ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY
                                                                                                                                                                                          spemcrkcsrcpsgevqvsnctswddiqcveefganatvetpaaeetmntspgtpapaae
                                                                                                                                                                                                                                          ehtgacnpctegvdytnasnnepscfpctvcksdqkhkssctmtrdtvcqckegtfrnen
                                                                                                                                                                                                                                                        EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN 120
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                                    standard;
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97US-0035496.
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142..148
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                                  Protein;
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Pred. No. 2
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es 0;
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This polypeptide comprises human Apo-2DcR, a novel member of the tumour necrosis factor receptor family that binds to Apo-2 ligand. Its amino acid sequence was deduced from the nucleotide sequence of an isolated cDNA clone (see AAV84347); an alternative translation
        than
               initiation site in this clone will encode a polypeptide (see AAW88409) comprising amino acid residues -40 to 269 of Apo-2DcR. Apo-2DcR shows more sequence identity to DR4 (60%) and Apo-2 (50%)
                                                                                                             New Apo-2DcR polypeptide - used for modulation apoptosis, e.g. in neurodegeneration
                                                                                                                                                                    Ashkenazi AJ,
Kim KJ, Wood
                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                           Claim 1;
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       to other apoptosis-linked receptors.
                                                                                                                                                   1999-095340/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apo-2DcR protein (amino acids 1-259).
                                                                                                                                         AAV84347
                                                                                          Page 50-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human;
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                                                                                                                                                                              Baker
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177..191
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156
/note-
169
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140
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77
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207..2
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192..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis; tumour necrosis factor receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; inflammation;
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                                                                                         88pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "extracellular domain, this domain specifically claimed in Claim 5"
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                                                                                                                                                                                                                                                                                           "N-glycosylation"
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99999999999999
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Apo-2DcR, or chimeras comprising Apo-2DcR or its (claimed) extracellular domain fused to a heterologous polypeptide are used to modulate apoptosis of mammalian cells (claimed) and/or NF-kappaB activation by Apo-2 ligand, and may be expressed in vivo or ex vivo for gene therapy. They can be used in methods for the modulation and diagnosis of apoptosis e.g. in cases of neurodegeneration, autoimmune diseases and inflammation. Most human tumour cells do not express Apo-2DcR transcripts, but normal tissues do, suggesting that Apo-2DcR may permit selective killing of cancer cells by Apo-2 ligand, possibly by protecting normal, but not cancerous, cells.
01-DEC-1999

01-DEC-1999

02-DEC-1999

02-DEC-1999

02-DEC-1999

16-DEC-1999

16-DEC-1999
                                                                                               01-DEC-2000;
                                                                                                                      07-JUN-2001.
                                                                                                                                             WO200140466-A2
                                                                                                                                                                                           adipocyte; A-peptide;
                                                                                                                                                                                                        cartilage;
                                                                                                                                                                                                                    breast;
                                                                                                                                                                                                                                                                              24-OCT-2001
                                                                                                                                                                                                                                                                                                                            AAU12321 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 secretory and transmembrane; PRO; mammalian; cancer; lung; t; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; lage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
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                                                                                                                                                                                                                                                      polypeptide sequence.
                                                                                               2000WO-US32678
99WO-US28301.
99WO-US28634.
99WO-US28551.
99WO-US28564.
99WO-US28565.
99US-0170262.
99WO-US30095.
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                                                                                                                                                                                          proliferation; gluce factor VIIA;
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61 61

Query Match Best Local Matches

Similarity

100.0%;

Score 1382; Pred. No. 2 Mismatches

DB 22; 2.5e-86; ~~ 0;

Length

0;

Gaps

0

60 60 Conservative

0;

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ANUI2172-ANUI2446 represent novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. CS come of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (TNF alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or cg ene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood cmonocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide confocules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, cc transgenic or knock out animals and can be used in gene therapy.
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20-DEC-1999;
30-DEC-1999;
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01 - WAR - 2000;

20 - MAR - 2000;

21 - MAR - 2000;

31 - MAR - 2000;

31 - MAY - 2000;

22 - MAY - 2000;

30 - MAY - 2000;

02 - JUN - 2000;
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06-JAN-2000;
11-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                        lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith
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24-FEB-2000;
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18-FEB-2000;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-2000;
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DB; AAS21393.
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99WO-US30999.
99WO-US31243.
2000WO-US00277.
2000WO-US03565.
2000WO-US04341.
2000WO-US04414.
2000WO-US04414.
2000WO-US04914.
2000WO-US04914.
2000WO-US05004.
2000WO-US05004.
2000WO-US05004.
2000WO-US07377.
2000WO-US07377.
2000WO-US08439.
2000WO-US13705.
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2000WO-US13705.
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A, Godowski PJ, Gurney AL,
Tumas D, Watanabe CK, Wood
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7hang Z;
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New PRO polypeptides, nucleic acids and (ant)agonists, useful for
                                                                                                                    Wood
                                                                                                                                       Hillan KJ,
                                                                                                                                                            Ashkenazi AJ,
                                                                                                                                                                                                        (GETH ) GENENTECH INC
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                                                   AAF30053
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                                                                                                                                         Mark MR,
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rk MR, Marsters
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233..239
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154..160
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85..92
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72..78
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126..1
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240..257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cAMP- and cGMP-dependent protein kinase
phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                               "N-myristoylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "N-myristoylation site"
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                                                                                                                                    SA,
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                                                                                                                                    Goddard A,
Pitti RM,
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                                                                                                                                    Godowski PJ, Gurne
Tumas D, Watanabe
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CC comprising these proteins or their agonists are useful for increasing confiltration of inflammatory cells into a tissue of a mammal, consists are useful for increasing confiltration of T-lymphocytes in a mammal in response to an antigen. CC proliferation of T-lymphocytes in a mammal in response to an antigen. CC claimed compositions comprising a PRO polypeptide or its antagonist contact the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering contents and the disorder is selected from systemic lupus erythematosus, rheumatoid arrhritis, osteoarthritis, juvenile chronic arthritis, costeoarthritis, inflammatory bowel disease, chronic arthritis, granulomatous chronic active hepatitis, primary biliary cirrhosis, granulomatous chapatitis, antipamatory bowel disease (such as multiple sclerosis), autoimmune centropathy, whipple's disease, (auto)immune-mediated skin disease (such as bullous skin disease, (auto)immune-mediated skin diseases (such as bullous skin disease, capthema multiforme and psoriasis), and constantive granulomatory bowel diseases (such as graft rejection and graft-versus-host disease) (all claimed). CC diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed). CC claimed methods of diagnosing these discorders comprise detecting the lung and transplantation associated diseases (such and body of the PRO popund capable of inhibiting the expression of captantity of the prop
                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo-2DCR, a novel human immunomodulator (27 kDa, p1 4.84), as deduced from a human breast carcinoma cDNA clone (see AAF30053). Apo-2DCR shows homology to apoptosis-linked receptors of the tumour necrosis factor receptor family, such as DR4 and Apo-2. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO366. Claimed compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing sclerosis,
                                                                                                                                                                                                                                                            Sequence
                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   method of stimulating an immune response in a mammal using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 AA;
100.0%; ilarity 100.0%; Conservative (
                                          Score 1382; DB 22
Pred. No. 2.5e-86;
                                                                                                      22;
                                                                                           Length
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                                          etmntspgtpapaaeetmttspgtpapaaeetmttspgtpapaaeetmttspgtpasshy
                                                    ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY
                                                                                                                                ehtgacnpctegvdytnasnnepscfpctvcksdqkhkssctmtrdtvcqckegtfrnen
                                                                                                                                           EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN 120
lsctivgiivlivllivfv
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Best Local Similarity
                                                                                                                                                                                                                                                      are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoletic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polypucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding a TRID polypeptide, also referred to as tumor. necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15;
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                               apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wei Y,
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                                                  MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRS
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EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN
                                \verb|marip| ktlk five vivavll pvlays at targe evpqqtvapqqqrhs fkgeecpagshrs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 1; 285pp; English.
                                                                                                                                                                                              259
                                                                                                                                                                                                                             (d)
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US13515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          necrosis factor receptor 5 (TRID) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                             disorders; (c) diseases associated with cardiovascular disorders; and (e) viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0135164
                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor receptor 5; TRID; TNFR-5;
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                                                                                                         0;
                                                                                                                       Score 1382;
Pred. No. 2.
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                                                                                                         Mismatches
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                                                                                                     DB 22;
2.5e-86;
es 0;
                                                                                                       Indels
                                                                                                                                      Length
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                   angiogenic
                                                                                                                                                            30-NOV-1999,
02-DEC-1999,
                                                                                                                                                                                                                                                                                                                        05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                              WO200053753-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiac
                              genetic
                                                                                                   Godowski
                                                                                                           Ashkenazi
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                                                                                                                                                                                 30-NOV-1999
                                                                                                                                                                                          05-OCT-1999
                                                                                                                                                                                                    15-SEP-1999
                                                                                                                                                                                                                       08-SEP-1999
                                                                                                                                                                                                                                  01-SEP-1999;
                                                                                                                                                                                                                                           26-JUL-1999
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                                                                                                                                                                                                                                                                       02-JUN-1999
                                                                                                                                                                                                                                                                                  14-may-1999
                                                                                                                                                                                                                                                                                                      08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease; Huntington's disease; stroke; drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB53091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB53091 standard;
                                                                                                                                                                                                             15-SEP-1999
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                  isolated nucleic acid for producing a PRO polypeptide, etic disorders and treating cardiovascular, endothelial logenic disorders, such as atherosclerosis, wounds or ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spemcrkcsrcpsgevqvsnctswddiqcveefganatvetpaaeetmntspgtpapaae
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                                                           2001-090793/10.
DB; AAC97488.
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                                                                                F, Pitti
                                                                                                                               GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertrophy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                       2000WO-US00219.
                                                                                                   Gurney
                                                                                                                                                                                                 99US-0145698.
99WO-US20111.
99WO-US20594.
99WO-US21090.
99WO-US21547.
                                                                                                                                                                                                                                                                                                                                                                                                    transgenic
                                                                                                           Baker
                                                                                                                                                   99WO-US28564
99WO-US28565
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99WO-US28313.
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                                                                                        RM,
                                                                                                                                INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                atherosclerosis; osteoporosis; hypertn; diabetic retinonathmonia
                                                                                       KP, Ferrara N, Gerber H, Goddard A
AL, Hillan KJ, Kuo SS, Mark MR, M
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259
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                                                                                                                                                                                                                                                                                                                                                                                                              screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                 arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                        healing; cancer;
                                                                                                  Marsters
                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth;
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Claim 69; Fig

56; 293pp; English

encoding

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AAW76331
ID AAW7
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AC AAW7
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DT 11-J
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KW Tumc
KW arth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC expression of activity; diagnosing a cardiovascular, endothelial or CC angiogenic disorder, or a susceptibility to such a disorder by detecting CC mutations in a PRO gene, or the expression level of a PRO gene within a CC particular tissue; treating a cardiovascular, endothelial or angiogenic CC disorder via the administration of a PRO protein, PRO nucleic acid, or CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a CC ell growth, cardiac hypertrophy or PRO-induced angiogenesis via the CC administration of a PRO proteins, antibodies against pRO proteins, PRO proteins, an agonist or antagonist thereof. CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO CC agonists and PRO antagonists may be used as therapeutic agents to treat CC cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's CC disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic CC invention. PRO proteins to development and screening of potential collavention. The development and screening of potential of the present sequence represents a PRO protein of the collavention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
    Tumour necrosis related
arthritis; septicaemia;
                                                             Human tumour necrosis related receptor TR5.
                                                                                                          11-JAN-1999
                                                                                                                                                                                    AAW76331 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel human angiogenesis associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encod PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \verb"etmntspgtpapaaeetmttspgtpapaaeetmttspgtpapaaeetmttspgtpasshy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  spemcrkcsrcpsgevqvsnctswddiqcveefganatvetpaaeetmntspgtpapaae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ehtgacnpctegvdytnasnnepscfpctvcksdqkhkssctmtrdtvcqckegtfrnen 120
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                                                                                                                                                                                                                                                                                                                                                                                                             ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259;
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                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
receptor; TR5; human;
transplant rejection;
                                                                                                                                                                                                                                                                                             259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
  inflammation; autoimmune di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
  disease;
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Matches 259;

Similarity

100.0%;

Score 1382; DB 12, Pred. No. 2.9e-86;

Length

0;

0,

Conservative

0;

Sequence

B

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activity comprises administering an antagonist to the polypeptide, administering a nucleic acid that inhibits the expression of the nucleotide sequence encoding the polypeptide and/or administering a polypeptide that competes with the polypeptide for its ligand, substrate or receptor. Diagnosing a disease or a susceptibility to a disease related to expression or activity of TR5 polypeptide, comprises determining the presence or absence of mutation in the nucleotide sequence encoding the TR5 polypeptide in the genome of the subject and/or analysing for the presence or amount of TR5 polypeptide expression in a sample. Identification of compounds which bind to TR5 comprises contacting host cells with a candidate compound and assessing the ability of it to bind to the cells. The active agents can be used for the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. oraff vs host disease, psoriasis), transplant rejection,
                                      graft vs host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restencis, brain injury, AII diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                protein that has a membrane proximal O-glycosylation region. The invention provides methods for the recombinant production of TR5 and its use in diagnostic and therapeutic methods. Treatment of a subject in need of enhanced TR5 activity comprises administering an agonist to the polypeptide and/or providing TR5 polynucleotide in a form so as to effect production of the polypeptide activity in vivo. Treatment of a subject with the need to inhibit TR5 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of human tumour necrosis related receptor TR5, as deduced from the sequence of an isolated cDNA clone (see AAV56990). The protein is characterised as a GPI-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases, infections, stroke, isohaemia, ARDS, psoriasis, restenosis, brain injury, AIDS and bone diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory bowel disease; graft versus host disease; infection; stroke; ischhemia; acute respiratory disease syndrome; psoriasis; restenosis; brain injury; AIDS; bone disease; cancer; atherosclerosis; Alzheimer's disease; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Fig 1; 22pp; English.
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N-PSDB; AAV56990.
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05-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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97US-0795910.
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66..299
/label=
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1..165
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RRESULT
AAY29864
ID AAYX
XX AAY2
XX DT 17-Y
XX THUME
XX HUME
XX HUME
XX HOME
XX L11-Y
PF 11-Y
XX L1-Y
PF 11-Y
XX L1-Y
PF 11-Y
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XX L1-Y
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XX L1-Y
PF 11-Y

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AAZ21093 to AAZ21102 encode new human secreted proteins and AAZ29861 t AAZ29873 represent the secreted proteins encoded by the polynucleotide sequences. AAZ21103 to AAZ21112 represent probes for the secreted proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity haematopoiesis regulating activity, tissue growth activity, haemostat activity, chemotactic/chemokinetic activity, haemostat
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14-MAY-1998;
10-MAR-1999;
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Merberg D,
                                                                                                                                                                                                                                                                                                                                                        Polynucleotides encoding secreted human proteins, derived from fetal brain, human adult blood, human adult bladder, or human and tissue cDNA libraries.
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McDonnell PC,

Young

PR,

(SMIK ) SMITHKLINE BEECHAM CORP

08-OCT-1997; 02-OCT-1998;

97US-0061334 98EP-0203332 EP911633-A1

Ношо

sapiens disease;

28-APR-1999

graft versus host disease; infection; stroke; i
acute respiratory disease syndrome; restenosis;

ischaemia;

respiratory disease synd lisease; atherosclerosis;

therapy

Tumour necrosis factor receptor; TR5; TRID; DcR1; agonist; antagonist; screening; human; cancer; AIDS; Alzheimer's dise; inflammation; arthritis; septicaemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection;

disease;

Tumour necrosis factor receptor TR5

19-JUL-1999

(first entry)

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                                                            autoimmune disease; viral infection; degenerative disorder; amyotrophic lateral sclerosis; retinitis pigmentosa; ischae cerebellar degeneration; myelodysplastic syndrome.
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   W09909165-A1
                               Homo sapiens
                                                                                                              Human; DR5; DR5s; TRAIL-R3; apoptosis related condition; cancer; therapy;
                                                                                                                                            Human TRAIL-R3 protein sequence.
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                                                                                ischaemic
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                                                                              injury;
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Matches

0;

Gaps

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CC This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An CC antibody against the TRAIL receptors is useful for detecting mammalian CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in CC bioassays for screening for (antiagonists of DR5 or TRAIL-R3 proteins. CC (Antiagonists identified by the assay are useful for modulating the CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial CC infarction and stroke). The polynucleotides can also be used to treat these diseases. Antisense oligonucleotides to the DNA sequences can be used to form a composition that is useful for inhibiting expression of a human DR5 or TRAIL-R3 protein.
                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 62-63; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newly isolated polynucleotide encoding a mammalian TRAIL receptor protein - useful in for screening for (ant)agonists that modulate the apoptotic activity mediated by DR5 or TRAIL-R3 proteins
                                                                                                         Sequence
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N-PSDB; AAX27280.
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                        Similarity
                                                                                                           299 AA;
100.0%; Score 1382; DB 20; ilarity 100.0%; Pred. No. 2.9e-86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM INC
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RESULT 11
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                                                                                                                                                                                                            EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN 120
                                   standard; Protein;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; TNF-related apoptosis-inducing ligand binding protein; clot TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy; thrombotic microangiopathy; thrombotic thrombocytopenic purpura; haemolytic-uraemic syndrome; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated TRAIL binding protein - which binds to a necrosis factor-related apoptosis inducing ligand, us diagnosis and treatment of TRAIL-mediated disorders
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 AAW88409 standard; Protein;
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                                                                   SPEMCRKCSRCPSGEVQVSNCTSWDDTQCVEEFGANATVETPAAEETMNTSPGTPAPAAE
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Pred. No. 2.9e-86;
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Key
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This polypeptide comprises human Apo-2DcR, a novel member of the tumour necrosis factor receptor family that binds to Apo-2 ligand. Its amino acid sequence was deduced from the nucleotide sequence of an isolated cDNA clone (see AAV84347); an alternative translation
                                        Claim
                                                       New Apo-2DcR polypeptide - used for apoptosis, e.g. in neurodegeneration
                                                                              WPI; 1999-095340/08
N-PSDB; AAV84347.
                                                                                                                                             18-JUN-1997;
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neurodegeneration; autoimmune disease; inflammation; cancer;
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                                                                                                                                                            12-JUN-1998;
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117
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247..261
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232..246
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217..231
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209
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196
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265..2
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262..2
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41..20
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224
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Best Local s
Matches 259
                                                                                                                                                                                UL144: death receptor: apoptosis; programmed cell death; FAS;
TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
(SCHE)
                          04-DEC-1998;
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                                                                                    15-JUN-2000
                                                                                                                WO200034335-A2
                                                                                                                                            HOMO
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Pred. No. 2.9e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A pure or recombinant polypeptide which binds to a polyclonal antibody specific for the mature UL144 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known, which include the CD95 (Fas/APO-1), the TNF receptor-6 (DR-6), and TNF-related protein (TRAMP), death receptor-6 (DR-6), and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
                                                                                       developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disea cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
                                                                            apoptosis;
                                                                                                                         Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
                                                                                                                                                                        18-JUN-1999
                                                                                                                                                                                             AAW93578;
                                                                                                                                                                                                                   AAW93578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page
                                                      Homo sapiens
                                                                                                                                                Human hAPO9 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                             human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide for modulating apoptosis to an antibody specific for UL144 or 1
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Pred. No. 2.9e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC This invention describes isolated Tumor Necrosis Factor (TNF) family CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active CC fragments, and isolated TNF related ligands I and 3 (TNRL1 and TNRL3) or CC their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic CC molety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of CC agents to the polypeptide/active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/ active fragments are also useful for screening CC arguments and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active considerative fragments and APO4 signal transducer molecules that specifically interact with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vitro. APO9 polypeptides are also identified using a change in level of APO4 care all useful as immunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transfected to human breast carcinoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
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                AAY05726
                                              AAY05726 standard;
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DB; AAX23412.
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                                            Protein;
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Pred. No. 6.3e-86;
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a putative glycosylphosphatidylinositol-anchored protein, which is ceither cell-associated or processed and secreted. Secreted TRAIL-R3 competes for the binding of TRAIL to TRAIL-R1 and/or TRAIL-R2, thereby acting as an inhibitor of apoptosis. Expression of TRAIL-R3 is restricted to peripheral blood lymphocytes and skeletal muscle. It is likely that TRAIL-3 acts as an important regulator of TRAIL-R2 and -R3 induced cell death in vivo. A method for preventing or reducing the advancement, severity or effects of an immunological disease involves administering a TRAIL-R2 or TRAIL-R3 blocking agent such as a soluble TRAIL-R (preferably comprising a human immunoglobulin Fc domain) and an antibody. A method of treating cancer involves administration of antibodies against TRAIL-R3 or TRAIL-R2. A method of inducing cell death involves administration of an agent capable of inhibiting the binding of TRAIL-R2 or -R3 to its ligand.
Query Match
Best Local Similarity
Matches 258; Conserv
                                                                                                                                                                                                                                                                         The present sequence represents TRAIL-R3, a novel mammalian cysteine-rich receptor of the tumour necrosis factor receptor The invention is related to novel receptors for TRAIL, i.e. TR (see AAY05725) and TRAIL-3. TRAIL-3 is highly glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-276942/23
N-PSDB; AAX25349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor receptor TRAIL-R3
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                                                                                                                                                                                                                                                                                                                                        Disclosure;
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12-SEP-1997;
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                                                             Sequence
                                                             259
                                                                                                                                                                                                                                                                                                                                        Page 28;
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97US-0058631.
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207..2
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25..259
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"TAPE
           99.5%;
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           Score 1375; DB 20
Pred. No. 7.4e-86;
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                      20;
                        Length 259;
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TRAIL-2
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Conservative

0;

Mismatches

Indels

0

Gaps

Search completed: August 13, 2002, 08:31:29 Job time: 123 sec

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Total number of hits satisfying chosen parameters:
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Perfect score:
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                                 283138 seqs,
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                                                                                                                                                                                                                                                                                         Copyright
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                                 96089334 residues
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880.337 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being primand is derived by analysis of the total score distribution. printed,

Database

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Minimum

Maximum

DB Bd

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length:

length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

## SUMMARIES

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10.1				10.2			10.4	10.4	10.5	10.6	10.7	10.8	11.1	11.3	11.4	11.8	11.8	11.9	12.0	12.0	12.0	12.3	12.9	13.4	13.6	13.9	14.5	14.6		Query
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S48478	в43692	JC5486	D36858	D72175	T28623	S24169	H81072	GQMST1	I48854	B38634	GQHUT1	A42086	JC2395	F36791	GQVZML	A46484	A40036	I37383	I48700	I37552	S12783	A35356	T29018	JN0006	JC4302	JC7705	A26431	GQHUN		TD
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126 9.1 138 2 D96715 126 9.1 514 2 A31643 126 9.1 571 2 T43456	9.2 1459 2 9.2 1802 2	9.3 393 2 9.2 135 2	9.4 461 1	9.4 88 2	9.4 1506 2	9.6 3020 2	9.6 607 2	9.6 307 1	9.6 888 2	9.7	9.7 93 2
222	N N	N N	1	N	2	N	N	_	N	N	N
D96715 A31643 T43456	T32271 S69703	S62335 T49996	GQRTT1	S02720	T30886	A43932	S27776	GSFF3	T46726	A60501	S04157
protein F4N2.10 (i cell adhesion 80K hypothetical prote	hypothetical prote HKR1 protein precu	I71-7 protein - fr AtAGP4 - Arabidops	tumor necrosis fac	outer membrane pro	intequmentary muci	mucin 2 precursor,	80K protein (allel	salivary glue prot	secreted acid phos	thrombomodulin pre	outer membrane pro

## ALIGNMENTS

nerve growth factor receptor precursor, low affinity [validated] - human N;Alternate names: NGF receptor C;Species: Homo sapiens (man)

C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 08-Dec-2000 C;Accession: A25218; A60204; S21689; I57638 R;Johnson, D; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.;

Cell 47, 545-554, 1986
A; Title: Expression and Structure of the human A; Reference number: A25218; MUID:87051725
A; Accession: A25218 n, D.; Lanahan, A.; 545-554, 1986 NGF receptor. Mercer, E.; Bothwell,

A; ACCESSION.... A; MOLECULE type: mRNA A; Residues: 1-427 <JOH> A; Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205 A; Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205 A; Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205 S Grob,

R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human A;Reference number: A60204; MUID:87085574
A;Accession: A60204 melanoma nerve growth fa

A;Molecule type: protein A;Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>A;Experimental source: melanoma cell line A875

follow the

nucle

A;Note: this sequence has been corrected by a note added in proof to R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H. Arch. Biochem. Biophys. 294, 244-252, 1992

A;Title: Structural domains of the extracellular domain of human nerve growth factor A;Reference number: S21689; MUID:92198017 A;Accession: S21689

A; Status: preliminary

A; Molecule type: protein
A; Residues: 183-208 <VIS>
R; Sebgal, A; Patil, N; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
Mol. Cell. Biol. 8, 3160-3167, 1988
A; Title: A constitutive promoter directs expression
A; Reference number: 157638; MUID: 89965903
A; Accession: 157638 of. the nerve growth factor recept

A; Molecule type: DNA A; Residues: 1-22 < RES> A; Status: preliminary; translated from GB/EMBL/DDBJ

A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207 C;Comment: This receptor is found on sensory and sympathetic neurons, on C;Comment: The cysteine-rich region of the extracellular domain may form C;Comment: This protein is thought to form a high-affinity receptor when C;Comment: This receptor undergoes both N- and O-linked glycosylation. C;Genetics: n part or all it associate

A; Gene: GDB: NGFR

A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprote: F;1-28/Domain: signal sequence #status predicted <SIG> neterodimer; monomer; phosphoprotein; predicted <SIG> receptor

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A;Cross-references: GB:X61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma C;Comment: The cysteine-rich region of the extracellular domain may form part or all of C;Comment: This protein is thought to form a high-affinity receptor when it associates C;Cenetics:
C;Genetics:
A;Introns: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Superfamily: nerve growth factor receptor; NGF receptor; P;1-29/Domain: signal sequence #status predicted <SIG>
F;1-29/Domain: signal sequence #status predicted <SIG>
F:1-29/Domain: signal sequence #status specifical sequence #status specifical sequence #status s
   F;30-425/Product: nerve growth factor receptor #status
F;30-251/Domain: extracellular #status predicted <EXT>
F;33-66/Domain: NGF receptor repeat homology <NG1>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-148/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation A;Reference number: PH1229; MUID:93077038
A;Accession: PH1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nerve growth factor receptor precursor, low affinity - rat N;Alternate names: NGF receptor C;Species: Rattus norvegicus (Norway rat) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change C;Accession: A26431; PH1229
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A; Residues: 1-20 <MET>
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A;Cross·references: GB:X05137; NID:g56755;
R;Metsis, M.; Timmusk, T.; Allikmets, R.; S
Gene 121, 247-254, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Gene transfer and molecular cloning A; Reference number: A26431; MUID:87115859 A; Accession: A26431
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117 124

63

CTKSTLRECSPCPDGT-FTKHENGIERCHPCRKPCELPMIEKTHCTALTDRECTCLSGTF 123

----NENSPEMCRKCSRCPSGEV--QVSNCTSWDDIQCVEEF 153

-TGACNPCTEGVDYTNASNNEPSCFPC-TVCKSDQKHKSSCTMTRDTVCQCKEGTF 116

QINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFSDVPSSVMKCKTYTD--C---F

G

Matches Query Match Best Local

68;

Conservative

35 ;

Length 651 Indels

72;

Gaps

12;

Local

Similarity

14 IVAVLLPVLAYSATTARQEEVPQQTVA------PQQQRHSFKGEECPAGSHRSEH

VLAAVLPLLVFLGTADAQPKLTSEQNAVSLPAGKYLHLDRATNQELICDKCPAGTYVSKH

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F;332-350/Domain:
F;410-475/Domain:
F;551-651/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           death receptor-6 - chicken

C;Species: Gallus gallus (chicken)

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change
C;Accession: JC7705

R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
                                                                                                                                                                                                                                                                        C;Comment: This receptor, a member of the tumor necrosis tresia, activates a cell death and/or survival signaling
                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine
A;Reference number: JC7705; MUID:21308433; PMID:11414698
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F;252-273/Domain: transmembrane #status predicted <NEM>F;274-425/Domain: intracellular #status predicted <NT>F;61/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                  F;1-21/Domain: signal sequence #status predicted <SIG>F;52-196/Domain: extracellular cysteine-rich, ligand-binding
                                                                                                                                                                                                           C; Keywords: ovary
                                                                                                                                                                                                                                     A;Gene: dr-6
                                                                                                                                                                                                                                                    C; Genetics
                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AF349908
                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-651 <BRI>
                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC7705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEVGSGLVFSCQDKQNTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQLRECTPWADAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDNVTFSDVVSATEPCKPCTECLGLQSMSAPCVEADDAVCRCAYGYYQDEETGHCEACSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLLILGVSSGGAK-----ETCSTGLYTHS--GECCKACNLGEGVAQPCGANQTVCEPC
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                                                                                                                         transmembrane #status predicted <TMM>
death domain #status predicted <DED>
                                                                                                          conserved
                     13.9%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%;
23.9%;
                                                                                                     cytoplasmic #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---QCKEGTFRNE-NSPEMCRKCSRCPSGEVQVSNCTSWDDIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
Score 192; DB 2;
Pred. No. 0.00015;
5; Mismatches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
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No. 3.4e-05;
                                                                                                     predicted
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                                                                                                                                                                                                                                                                          cascade
                                                                                                                                                                                                                                                                                                factor receptor
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                                                                                                                                                                    #status
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                                                                                                                                                                    predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
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                                                                                                                                                                                                                                                                                             family,
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                                                                                                                                                                    <ECL>
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F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NGI>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;84-126/Domain: NGF receptor repeat homology <NGF>
F;361-421/Domain: signal transduction #status predicted <TMM>
F;361-447/Domain: signal transduction #status predicted <SIT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor receptor p55 precursor - pig C;Species: Sus scrofa domestica (domestic pig) C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999 C;Accession: JC4302; pc4093 R;Suter, B.; Pauli, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the A;Reference number: JC4302; MUID:96011645
A;Accession: JC4302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-7 <SU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U19994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-461 <SU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                    213
                                                                                                                                                                                                                                                   153
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    333
                                           237
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                                                                                                                                                                                                                                                                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                     37
- ES
                                         SS
                                                                                                                                                                                                                                                                                                                                                           SNNEPSCFPCTVCKSD--QKHKSSCTMTRDTVCQCKEGTFRNENSPEM--CRKCSRCPSG 134
                                                                                                                                                                                                                                                                                                                                                                                                                 REKRESL - - - - CPQGKYSHPQNRSICCTKCHKGTYLHNDCLGPGLDTDCRECDNGTFTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQQRHSFKGEECPAG--SHRSEHTGACNPCTEGV----
                                                                               FSPIPSFSPTTTFSPVPSFSPISSPTFTPCDWSNIKVTSPPKEIAPPPQGAGPILPMPPA 332
                                                                                                                           -TPAPAAEETMTTSP--
                                                                                                                                                                                                                                                 TVQLPCLEKQDTICNCHSGFFLRDKECVSCVNCKNADCKNLCPATSETRNDFQDTGTTVL 212
                                                                                                                                                                                                                                                                                      EVQ-----VSNCTSW-----DDIQCVEEFGANATVETPAAEETMN------
                                                                                                                                                                                                                                                                                                                                 ENHLTQCLSCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFDLSSSPAP----RVSNGTAEPTVDYNDTSANGTVGAPGSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKNMVVVKPGTKESDNVC-XSPASLPNTSLTSS----DAQADGETYEAPPTAYLPKGLNSS
                                                                                                                                                                    LPLVIFFGLCLAFFLFVGLACRYQRWKPKLYSIICGKSTPVKEGEPEPLATAPSFGPITT、272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-461 <SUT>
                                           238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC4093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID:g1141752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 188.5; DB 2
Pred. No. 0.00018;
0; Mismatches 94
                                                                                                                           -GTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             porcine
                                                                                                                                                                                                        TSPGTPAPAAE-ETMNTSPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: AAC48499.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DYTNA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor receptor.
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R;Large, T
Neuron 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: JN0006: A60504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom C;Comment: The cysteine-rich region of the extracellular domain may form part or all C;Comment: This protein is thought to form a high-affinity receptor when it associate C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF
A;Reference number: A60504; MUID:90152140
A;Accession: A60504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Heuer, J.G.; Fatemie-Nainie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: embryonic chick brain R; Heuer, J.G.; Fatemie-Nainie, S.; Wheeler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: JN0006; MUID: 90166579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nerve growth factor receptor, low affinity precursor - chicken N; Alternate names: NGF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;52/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-416 <LAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262-416/Domain:
  217
                                                  203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 VAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEEC------PAGSHRSEHT 63
                                                                                                                                                                                                                                                                                                                                                                                                                           σ
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                                               GTPAPAAEETMTTSPGTPAPAAEETMTTSPGT-----PASSHYLSCTIVGIIVLI 252
                                                                                                                                                                                                             CKECSICEVGFGLMFPCRDSQDTVCEECPEGTFSDEANFVDPCLPCTICEENEVMVKECT 173
                                                                                                                                                                                                                                                                                                                                                                                                                           VPLLLLLPAGPTWGSKEKC-----LTKMYTTSGECCKACNLGEGVVQPCGVNQT---
                                                                                                    ATSDAEC-RDLHPRWTTHTPSL----AGSDSPEPITRDPFNT
                                                                                                                                                      SWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSP 202
                                                                                                                                                                                                                                                                                                                                                                      GACNPCTEGVDYTNASNNEPSCFPCTVC-----KSDQ-----
                                                                                                                                                                                                                                                                                                                 -VCEPCLDSVTYSDTVSATEPCKPCTQCVGLHSMSAPCVESDDAVCRCAYGYFQDELSGS 113
-----LADIVTTVMGSSQP-----VVSRGTADNLIPVYCSILAAVVVGLVAYI
                                                                                                                                                                                                                                                               -KHKSSCTM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane #status predicted <MEM>
intracellular #status predicted <INT>
                                                                                                                                                                                                                                            ----TRDTVC-QCKEGTFRNE-NSPEMCRKCSRCPSGEVQVSNCT 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 184.5; DB 1
Pred. No. 0.00029;
6; Mismatches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.J.; Misko, T.P.; Shooter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #text_change 10-Sep-1999
                                                                                                      ------EGMATT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nerve growth factor receptor i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97;
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                                                                                                         216
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hypothetical protein ZK84.1 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #C;Accession: T29018

15-Oct-1999 #text\_change 17-Mar-2000

submitted to the EMBL Data Library, April A;Description: The sequence of C. elegans

1995 cosmid R;Kirsten,

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A;Title: Two human TNF receptors have similar A;Reference number: A48416; MUID:91370690 A;Accession: A48416
                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186 R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990 A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A;Reference number: A36475; MUID:91045991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000 C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094 R;Smith, C. A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R. Science 248, 1019-1023, 1990 A;Title: A receptor for tumor necrosis factor defines an unusual family of carefore number: A35356; MUID:90260639
    A; Residues: 23-461 .
A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor necrosis factor receptor 2 precursor [validated]
N;Alternate names: 75K tumor necrosis factor receptor;
C;Species: Homo sapiens (man)
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A;Introns: 22/2; 45/3; 1
C;Superfamily: collagen
                                                    A;Molecule
                                                                             A;Status:
                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-461 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-801 <KIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 PAAEETMTTSPG----TPAPAAEETMTTSPG---TPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 SVPAPVADAAAGYDSPSSIPEETPAPAAEDTPAPASAAAEETPAPAPAAEETPAPETASA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 GVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTF-----RNENSPEMC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 AVLLPVLAYSATTARQEEVPQQTVAPQQQ----RHSFKGEECPAGSHRSEHTGACNPCTE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                             preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESATEAPSDSAAPIGPAASEPAPAPIEAPATDAATLETAPAPAAEPAPAAEAAAGYDAPS
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                                                 type:
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    GB:S63368;
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  NID: g235648;
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Pred. No. 0
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    PIDN: AAB19824.1;
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    human
    TNF receptor type

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PID:g235649
                                                                                                                                                distinct intracellular
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Db Db

150 181

122

PGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSSTDI-CR

-----VEEFGANATVET--PAAEETMNTSPGT---PAPAAEETMNTSPGTPAPAAEETM 198

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A; Molecule type: mRNA
A; Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A; Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
A; Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
A; Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
A; Cottscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, J. Biol. Chem. 265, 20131-20138, 1990
A; Title: Purification and partial amino acid sequence analysis of two distinct tumor A; Reference number: A23666; MUID:91056048
A; Accession: A23666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: duplication; glycoprotein; receptor; transmembl F;1-22/Domain: signal sequence #status predicted <SIG> F;23-416/Product: tumor necrosis factor receptor 2 #status F;40-76/Domain: NGF receptor repeat homology <NG1> F;78-119/Domain: NGF receptor repeat homology <NG2> F;78-119/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Nolecule type: protein
A; Residues: 23-40;65-69;136-141;300-306
A; Residues: 23-40;65-69; Mallach, D.
Qy
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A; Residues: 1-37 < RES>
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A;Title: Cloning, sequencing and partial functional characterization of the A;Reference number: 138094; MUID:95121934
A;Accession: 138094
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A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and A;Reference number: A36007; MUID:90349572
A;Accession: A36007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F; 262-279/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;164-201/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;120-162/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:125914; A; Map position: 1p36.2-1p36.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 27-31 <ENG>
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                                                                                                                                                                                                                                                                                                                                                                                                             ;280-461/Domain:
;171,193/Binding
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                   Query Match
Best Local
        113
                                                             64
                                                                                                                 59
                                                                                                                                                                                                                     11 VVVIVAVLLPVLAYSATTARQEEVPQQTVAPQ-----
                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                   4
        EGTFRNENSPEMCRKCS---RC--
                                                                                                                                                                   VAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHA 63
                                                             KVFCTKTSDT-VCDSC-EDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCR 121
                                                                                                               ----RSEHTGACNPCTEGVDYTNASNNEPSCFPC-TVCKSDQKHKSSCTMTRDTVCQCK 112
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                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       NGF receptor repeat homology <NG3>
NGF receptor repeat homology <NG4>
transmembrane #status predicted <TMN>
intracellular #status predicted <INT>
site: carbohydrate (Asn) (covalent) #:
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                                                                                                                                                                                                                                                                                                      12.3%;
22.3%;
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                                                                                                                                                                                                                                                                                                   Score 169.5; DB Pred No. 0.0025;
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                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                          123;
                                                                                                                                                                                                                     -----QQRHSFKGEECPAGSH- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane
     -PSGEVQVSNCTSWDDIQC- 149
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RESULT 9
137552
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Ante: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Anccession: 137552
R;Latza, U; Durkop, H; Schnittger, S; Ringeling, J; Eitelbach, F; Hummel, M.;
Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignm
A;Reference number: 137552; MUID:34170844
A;Accession: 137552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: nerve growth factor receptor homolog C; Species: Rattus norvegicus (Norway rat) C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text C; Accession: $12783; $08036 R; Mallett, S.; Fossum, S.; Barclay, A.N. EMBO J. 9, 1063-1068, 1990 A; Title: Characterization of the MRC OX40 antigen of act A; Reference number: $12783; MUID: 90214614 A; Accession: $12783
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S12783
OX40 ar
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                                                                                                                                                                      A;Cross-references: EMBL:X75962; NID:g472957; PIDN:CAA535
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-271 <MAL>
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                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-277 < RES>
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                                                                                       Local
                 ECPAGS-----HRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVC--KSDQKHKSSCTM 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDTVCQCKEGTF-RNENSPEMCRKCSRCPSGEVQVSN---CTSWDDIQCVEEFGANATVE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECQPGHGMVSRCDHTRDTVCHPCEPG--FYNEAVNYDTCKQCTQCNHRSGSELKQNCTPT
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                                                                 . Similarity
59; Conserv
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28.4%;
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                                                              Score 166.5; DB 2;
Pred. No. 0.0024;
6; Mismatches. 83;
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RESULT
I37383
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R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B ce A;Reference number: 148700; MUID:94044750
A;Accession: I48700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Gene structure and chromosomal localization of the mouse homologue of A;Reference number: I48334; MUID:95255413
A;Accession: I48334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C;Accession: 148700; 148334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; N
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A; Residues: 1-14, 'G'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene ox40 protein - mouse N;Alternate names: OX40 antigen
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C;Superfamily: CD27 antigen; NGF receptor repeat homology
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216 LLGLGLGLLAPLTVLLALYL 235
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                                                                                                                                                                                                                                                                             66 CNPCTEGVDYTNASNNEPSCFPCTVC--KSDQKHKSSCTMTRDTVCQCKEGTF-RNENSP 122
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                                       YLSCTIVGIIVLIVLLIVEV
                                                                                                                                                                   KLGVDCVPCPPGHFSPGNNQACKPW
                                                                                                                                                                                                          EMCRKCSRCPSGEVQVSN----CTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAA 179
                                                                                                                                                                                                                                                    CHPCETG - - FYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGY
                                                                                                                                                                                                                                                                                                                                    ALLLLALTLGVTARRLNCV-----KHTYPSGHKCCRECQPGHGMVSRCDHTRDTL
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                                                                                 LDAVCEDRSLLATLLWETQRP---TFRPTTVQSTTVWPRTSELPSPPTLVTPEG-PAFAV
                                                                                                                    EETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSH
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EMBL:X85214;
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25.8%;
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                                       259
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 166; DB 2;
Pred. No. 0.0026;
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apoptosis-mediating surface antigen Fas precursor -human N;Alternate names: surface antigen APO-1 C;Species: Homo sapiens (man) C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000 C;Accession: A40036; S24543; A38142 R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshir
              A; Molecule type: nucleic acid
A; Residues: 1-134, 'Q', 136-335 <OEH>
A; Experimental source: SKM6.4 cells
A; Note: sequence extracted from NCBI backbone (NCBIP:103810)
A; Note: in NCBI backbone the source is designated as mouse
                                                                                                                                                             A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742 R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; J. Biol. Chem. 267, 10709-10715, 1992 A;Title: Purification and molecular cloning of the APO-1 cel A;Reference number: A38142; MUID:92268122 A;Accession: A38142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 66, 233-243, 1991
A;Title: The polypeptide encoded by the cDNA A;Reference number: A40036; MUID:91309137
A;Accession: A40036
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A40036
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A;Residues: 1-335 <ITO>
A;Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1;
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A;Title: Three functional soluble forms of the A;Reference number: 137383; MUID:95181785
A;Accession: 137383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAS soluble protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I37383
                                                                                                                                       A; Status: preliminary; not compared with
                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-335 < KRA>
                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S24543
                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, February A; Reference number: S24543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              日
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g695539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-314 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 KENQGSHESPTLNPETVA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLPVLAYSATTARQEEVPQQ-----TVAPQQQRH-----SFKGEECPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PAAEETMNTSPGTPA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKCRCKPNFFCNSTVCEHCDPCTKCEHGIIK--ECTLTSNTKCKEEVKRKEVQKTCRKHR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVET---- 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLC--DEGHGLEVEINCTRTQN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHRSEHTGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGLHHDGQFCHKPCPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- CNPCTEGVDYTNASNNEPSCFPCTVCKSDQKH----KSSCTMTRD 106
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24.2%;
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Pred. No. 0.0035
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                                                                                                                                                                                                               of the APO-1 cell surface
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                                                                                                                                          translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis-inducing Fas molecule
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                                                                                                                                                                                                                                                         Klas, C.; Li-Weber, M.; Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g182410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
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108

58 64

KKVEDCKMNGGTPTCAPCTEGKEYMDKNHYADKCRRCTLC - - DEEHGLEVETNCTLTQNT 121

HRSEH-----TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKH----KSSCTMTRDT 107

VCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGAN

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A:Map position: 10q24.1-10q24.1
C;Superfamily: NGF receptor repeat homology
C;Keywords: apoptosis; surface antigen; transmembrane |
F;1-16/Domain: signal sequence #status predicted <SIG>
F;85-128/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                             C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226 A;Experimental source: BAM3 macrophage cell line A;Experimental source: BAM3 macrophage cell line A;Note: sequence extracted from NCB backbone (NCBIN:81544, NCBIP:81545) R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S. Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993 A;Title: Aberrant transcription caused by the insertion of an early transcription caused by the insertion of an early transcription caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision
C;Accession: A46484; A47254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
A46484
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                                           Q
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A;Accession: A47254
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A;Map position: 10q24.1-10q24.1
C;Superfamily: NGF receptor repeat homology
                                                                                                                                                                                                                                                                                               C; Superfamily: NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                           A; Note:
                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; A;Experimental source: MRL lpr/lpr
                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: nucleic acid
A; Residues: 1-96 <ADA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-327 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: The cDNA structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis-mediating membrane-associated polypeptide Fas - mouse
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                                                                                                                        Query Match
Best Local
                                                                                                 Matches
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Best Local
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                                                14 IVAVLLPVLAYS------ATTARQEEVPQQTVAPQQQRHSFKG------EECPAGS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
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nes 43; Conser
                                                                                                                      Local Similarity
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  4
                                                                                                                                                                                                                                                                                                                           sequence extracted from NCBI backbone
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IWAVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCQPGK 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHRSEHTGA-----CNPCTEGVDYTNASNNEPSCFPCTVCKSDQKH-----KSSCTMTRD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKCRCKPNFFCNSTVCEHCDPCTKCEHGIIK--ECTLTSNTKCKEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1274-1279, 1992
                                                                                                 Conservative
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                                                                                                                      11.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , expression, and chromosomal assignment of the mouse Fas {\tt MUID:92148151}
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3.
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                                                                                                                      Score 163; DB 2;
Pred. No. 0.0045;
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                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insertion of an early transposable elem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change 05-Nov-1999
                                                                                                                                               Length 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                                                           NCBIN: 126853,
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                                                                                                 30;
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                                                                                            Gaps
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RESULT 14
GOVANL
GOVANL
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A4056
R;Upton, C:; Macen, J.L.; Schreiber, M.; Mcfadden, G.
Virology 184, 370-382, 1991
A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis
A;Accession: A40566; MUID:91335768
A;Accession: A40566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
F36791
C;Species: ictalurid herpesvirus 1 (strain auburn 1)
C;Species: ictalurid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 31-Jan-2000
C;Accession: F36791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                          Virology 186, 9-14, 1992
A;Title: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A39447; MUID:92087490
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Davison, A.J.
submitted to GenBank, January 1992
A;Description: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A36804
A;Accession: F36791
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                                                                                                                                                           A;Gene: 50
C;Superfamily: period clock protein; EGF homology
                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                              R; Davison, A.J.
                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-670 <DAV>
A;Cross-references: GB:M75136; NID:g331209; PIDN:AAA88153.1; PID:g331260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-326 < UPT>
                                                                                                                                                                                                                                                     A; Note: neither protein nor nucleic acid sequence is
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155 ANATVETPA-AEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETM 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 ETCTSSFNYISVEFNLYPVNDTSCTTTAGPNEVVKTSEFSVTLNHTDCDP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 RVCDCSAGNYCLLKGQEGCRICAPKTKCPAGYGVSGHTRTGDVLCTKCPRYTYSDAVSST 161
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                                                    15;
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Search completed: August 13, Job time: 38 sec 2002, 08:30:04

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T116_RAT
TNR6_PIG
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TR16_CHICK
TR1A_BOVIN
TR16_CHICK
TR1A_HUMAN
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VC22_VARV
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AMTH_YEAST
TRBM_MOUSE
CC31_CHOCK
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O77736 sus scrofa
P51867 bos taurus
P18519 gallus gall
C19131 bos taurus
P20333 homo sapien
P15725 rattus norv
P43489 homo sapien
P25445 homo sapien
P25445 homo sapien
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P29827 myxoma viru
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O63199 rattus norv
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P15306 mus musculu
P34015 variola vir
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P34015 variola vir
P35045 gallus gall
P02840 drosophila
P11910 neisseria g
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Degli-Esposti M.A.,
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., CHARACTERIZATION, TISSUE=Foreskin fibroblast, and Perip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baldwin D., Yuan J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marsters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98044290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNFRSF10D OR DCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T10D_HUMAN
                                                                                                                                                                                                                                                        Immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashkenazi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TRAIL receptor-4)
                                                                                                                                                                                                                   EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
        IL SIGNALING
S Lett. 424:41-45(1998).

S Lett. 424:41-45(1998).

FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains truncated death domain and hence is not capable of inducing apoptosis but protects against TRAIL-mediated apoptosis. Regare contradictory with regards to its ability to induce the are contradictory with regards to ref.1 it cannot but according
      kappaB
ref.2 i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSCTIVGIIVLIVLLIVFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN
                                                                                                                                   signalling.";
                                                                                                                                                                                                                                                                                                                R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                        7:813-820(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.A.,
                                                                                                                                                                                                                   FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                 ceptor for Apo2L/TRAIL
7:1003-1006(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human)
                                                                                                                                                                                                               N.A.,
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kel. 40, Last annotation update)
kel. 40, Last sequence update
kel. 40, Last sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheridan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                   PubMed=9537512;
G.-L., Wei Y.-F., Dixit V.
mber of the TRAIL receptor
                                                                                                                                                                                                                                                                                                                                PubMed=9430226;
., Dougall W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9382840;
eridan J.P., Pit
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(According to ref.)
                                                                                                                                                                                                                   AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1382;
Pred. No. 7.4
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pitti R.M.,
                                                                                                                                                                                                                                                                                                                                                                     ATION, AND VARIANTS
Peripheral blood ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRUNDD
                                                                                                                                                                                                                                                                                                                                Smolak P.J.,
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. No. 7.4e-78;
smatches 0;
                                                                                                                                                                             Dixit V.M.;
                                                                                                                                                                                                                                                                          B NF-kappaB
DS an incomp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386
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l A.D., Gc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
                                                                                                                                                                                                                                                                          incomplete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
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                                                                                                                                                         family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski
                                                                                                                                                                                                                                                                                                                                  Waugh J.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Α.,
                                                                                                                                                                                                                                                                                                                                                                       lymphocytes;
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eath doma
                                                                                                                                                                                                                                                                                                                                                                                         S-35
                                                                                                                                                         that antagonizes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skubatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                   death domain.";
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                                                                                                                                                                                                                                                                                                                                  Smith C
                                                                                                                                                                                                                                                                            against
lomain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00652; TNFR_NGFR_1; PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001368; TNFR_c6. pfam: PF00020; TNFR_c6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 603614;
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor;
 184
                       155
                                           125
                                                                95
                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 2 THER-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN (TRUNCATED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein TISSUE SPECIFICITY: Widely expressed, in parti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Widely expressed, in particular in fetal kidney, lung & liver and in adult testis and liver. Also expressed in peripheral blood leukocytes, colon and small intestine, ovary, prostate, thymus, spleen, pancreas, kidney, lung, placenta and
                                                              ACNPCTEGVDYTNAŚNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEM 124
NTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSC
                      CRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILG
                                 CRKC-SRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETM 183
                                                                                                         PKILKFVVFIVAVLLPVRVDSATIPRQDEVPQQTVAPQQQRRSLKEEECPAGSHRSEYTG
                                                                                                                             PKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF021233;
AF023849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF029761;
                                                                                                                                                   al Similarity
132; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P19438; 1NCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF021232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00020; TNFR_c6; SM00208; TNFR; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis;
                                                                                                                                                                                                        386
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; AAD03477.1; -.; AAC32765.1; -.; AAC32766.1; -.; AAC52053.1; -.
                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                386
386
                                                                                                                                                                                                        41823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Transmembrane; Repeat; Signal;
                                                                                                                                                             45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٧.
                                                                                                                                                                                                        ₩.
                                                                                                                                                    22;
                                                                                                                                                   Score 634; DB 1;
Pred. No. 2.9e-32;
2; Mismatches 41
                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
P -> S (IN TRAIL-R4-B).
FTIG=VAR_011417.
S -> L (IN TRAIL-R4-B).
                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                               TNFR-CYS
                                                                                                                                                                                                      S -> L (IN TRAIL-R4-B).
/FTId-VAR_011418.
77A93577CAAF2632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NN
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                                                                                                                                                                                                                                                                                                                                                                     (TRUNCATED).
                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                      Length 386;
                                                                                                                                                   Indels
                                                                                                                                                   Gaps
                                                                                                                             64
243
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               Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_C5; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PR0SITE: PS0017; DEAVH_DOMAIN; 1
PR0SITE: PS00152; TNFR_NGFR_1; 2.
PR0SITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION.

MEDLINE-98090092; PubMed-9430227;

Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Chaudhary P.M., a new member of the TNFR family, and DR4 i "Death receptor 5, a new member of the NF-kappaB pathway."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T10A_HUMAN
000220;
                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=97238921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor 4) (TNF-related apoptosis-inducing ligand
receptor-1) (TRAIL-R1).
                                                                                                                                                                 EMBL; U90875; AAC51226.1; HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FADD-dependent apoptosis and activate Immunity 7:821-830(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The receptor for the cytotoxic ligand Science 276:111-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan G., O'F
Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                                                                      InterPro; IPR001368;
                                                                                                                                   InterPro; IPR000488;
                                                                                                                                                                                                                            entities requires a
                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFRSF10A OR DR4 OR TRAILR1 OR APO2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 2 THER-CYS REPEATS SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                       factor kappaB-pathway and can bind the cytoplasmic ada molecule FADD/MORTI which engages initiator caspases s caspase 8 leading to subsequent activation of effector that execute apoptotic death of the cell.

SUBUNIT: Can interact with TRADD and RIP.
SUBCELULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Widely expressed. High levels are spleen, peripheral blood leukocytes, small intestine a but also in K562 erythroleukemia cells, MCF7 breast cacells and activated T-cells.
                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collab-
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Receptor for the cytotoxic ligand TRAIL; apoptosis in a caspase-dependent manner. Can trigg
                                                                                                                                                    603611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVVLVIILAVVVVGF 230
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email to license@isb-sib.ch).
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el. 40, Last annotation update)
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TISSUE-FORESKIN fibroblast;
MEDLINE-97459925; PubMed-9311998;
Walczak H., Degli-Esposti M.A., J.
Bolani N., Timour M.S., Gerhart M.
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                                          Screaton G.R., Mongkolsapaya McMichael A.J., Bell J.I.; "TRICK2, a new alternatively cytotoxic signal from TRAIL." Curr. Biol. 7:693-696(1997).
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                                                                                                                                                                                                                                                 Goodwin R.G., Rauch C.T.;
"TRAIL-R2: a novel apoptosis-mediating EMBO J. 16:5386-5397(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE FROM N.A. (SI Farrah T., Vu T., Gill "Homo sapiens homolog
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Submitted
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"Identification and molecular cloning cytotoxic ligand TRAIL.";
J. Biol. Chem. 272:25417-25420(1997).
         X-RAY CRYSTALLOGRAPHY (2.4 MEDLINE=20017054; PubMed=10 Hymowitz S.G., Christinger Kelley R.F., Ashkenazi A.,
                                                                                                                                                                                                            Arai T., Akiyama Y., Okabe S., Saito K., "Genomic structure and mutation analyses gene in colorectal carcinoma.";
                                                                                                                                                                                                                                                                                                                                                                Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray "Death receptor 5, a new member of the TNFR family, and I FADD-dependent apoptosis and activate the NF-kappaB pathw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLINE-97467719; PubMed-9326928; Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;
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"Characterization of two recepters Lett. 416:329-334(1997).
                                                                    Strausberg
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"Control of TRAIL-induced
receptors.";
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MEDLINE=97390509; F
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MEDLINE=98090092; Pubmed=9430227;
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G., Ni J., Wei Y.-F., Yu G.-I.,
antagonist decoy receptor and a
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RE=97390509; PubMed=9242611;

dan J.P., Marsters S.A., Pitti R.M., G
in D., Ramakrishnan L., Gray C.L., Bak
in D., Godowski P., Ashkenazi A.;
rd A.D., Godowski P., Ashkenazi A.;
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Zhang
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death
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Baker K.,
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                                                                                                                     factor receptor.";
                                                                                                                                O'Hara
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                    Ultsch M.,
                                       54-183
                                                                                                                                                                                                                                                                                   family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R., Dixit V.M.;
domain-containing
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of
                                                                                                            databases.
                                                           databases
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                                                                                                                                                                                                                        ., Yuasa Y.
DR5/TRAIL
                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                       A., Skubatch
, Wood W.I.,
Apo2L/TRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meng
R., I
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                     O'Connell
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Hamilton
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InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_C6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM000208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICING.

-ITISSUE SPECIFICITY: Widely expressed in adult and fetal tissues; very highly expressed in tumor cell lines such as HeLa 53, K562, HL-60, SW480, A549 and G361; highly expressed in heart, peripheral blood lymphocytes, liver, pancreas, spleen, thymus, prostate, ovary, uterus, placenta, testis, esophagus, stomach and throughout the intestinal tract; not detectable in brain.

-I DISEASE: Defects in TWFRSF10B may be a cause of squamous cell carcinoma of the head and neck.

-I SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
the Euro
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                                                                                                                                                                                                                         EMBL;
EMBL;
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MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mongkolsapaya J., Grimes J.M., Jones E.Y., Screaton G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex with death receptor 5."; Mol. Cell 4:563-571(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of the TRAIL-DR5 complex reveals mechanisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates apoptosis in a caspase-dependent manner. Can trigger the nuclear factor kappaB-pathway and can bind the cytoplasmic adapter molecule FADD/MORTI which engages initiator caspases such as caspase 8 leading to subsequent activation of effector caspathat execute apoptotic death of the cell.

SUBUNIT: Homotrimer (Potential). Can interact with TRADD and SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS, A LONG FORM/TRICK2B (SHOW)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Encopean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content by non-profit institutions as long as its content.
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601400;
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                                                                                                                                                                                                                                                                                        AB014714;
AB014715;
AB014716;
AB014717;
AB014717;
AF153687;
AF192548;
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AB014711;
AB014712;
AB014713;
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AF012535;
AB014718;
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AF018658;
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                    PS50017;
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AAF07175
AAH01281
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AAB67109.1;
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AAB70577.1;
AAB70578.1;
AAB81180.1;
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AAB67103.
BAA33723.
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BAA33723
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TNFR_NGFR_1;
                    DEATH_DOMAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stuart D.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
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Best Local S
Matches 105
                                                                                                                                         ul-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
(P75 ICD) (Low affinity neurotrophin receptor p75NTR).
                                                                                                                                                                             TR16_HUMAN
P08138;
01-AUG-1988
01-AUG-1988
16-OCT-2001
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SEQUENCE OF 1-22;
MEDLINE=89096903;
Sehgal A., Patil I
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REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                    Johnson D., Lanahan A., Bu
Bothwell M., Chao M.;
"Expression and structure
Cell 47:545-554(1986).
                                                                        SEQUENCE FROM N.A. MEDLINE=87051725;
                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50050; TNFR_NGFR_2;
                                                                                                     NCBI_TaxID=9606;
                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing;
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211
232
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97
138
192
339
250
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116
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                                                                                                                                                                                                                     STANDARD;
                   FROM
 PubMed=2850481,
N., Chao M.;
                                                                          PubMed=3022937;
                                                                                                              Chordata;
Primates;
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231
440
137
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422
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179
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                   N.A
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                                                               Buck
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                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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Pred. No. 6.5e-21;
13; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC
TNFR-CYS 1.
TNFR-CYS 2.
TAPE.
DEATH.
                                                               C.R.,
                                               the
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                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-GLY.
                                                                                                                                                                                                                     PRT;
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                                               human
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                                                               Sehgal
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                                                                                                                                                                                                                     427
                                               NGF
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                                                               Α.,
                                                                                                               Hominidae;
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                                                               Morgan C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 440
                                                                                                                       Euteleostomi;
                                                                Mercer
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Best Local
                                            Matches
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InterPro; IPR001388; TNFR_C6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_C6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00008; TNFR; 3.
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                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                          REPEAT
REPEAT
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EMBL; M21621; AAA36363.1; -.
PIR; A25218; GQHUN.
HSSP; P07174; INGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE E INTERACTS WITH P75NTR-ASSOCIATED CELL DEATH EXECU SUBCELLURAR LOCATION: Type I membrane protein. PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: LOW AFFINITY RECEPTOR WHICH AND NT-4. CAN MEDIATE CELL SURVIVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEURAL CELLS
                     EECPAG - - SHRSEHTGACN - - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162010;
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EACPTGLYTHSGECCKACNLGEGVAQPCGANQTVCEPCLDSVTFSDVVSATEPCKPCTEC
                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.
                                                                                                                                                                                                                                                                                                                                                                                                     PS00652; TNFR_NGFR_1; 3. PS50050; TNFR_NGFR_2; 4. PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                              Neurogenesis;
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W AFFINITY RECEPTOR WHICH CAN
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                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis
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BY SIMILARITY.
                                          Score 201.5; DE Pred. No. 6e-06; Mismatches
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DEATH.
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TNFR-CYS 1.
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AR (POTENTIAL).
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Tumor necrosis factor receptor superfamily member 16 precursor (Low-
affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
(P75 ICD) (Low affinity neurotrophin receptor p75NTR)
NGFR OF THE SET 16.
EMBL; X05137; CAA28783.1; EMBL; X61269; -; NOT_ANNO PIR; A26431; A26431.
                                                               modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                 This
                                                                                                                                                                                                                                                           MEDLINE-97449145; PubMed-9305641; Liepinsh E., Ilag L.L., Otting G., "NMR structure of the death domain EMBO J. 16:499-5005(1997).
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93077038; PubMed=1446821;
Metsis M., Timmusk T., Allikmets R., Saarma M., Persson H.;
"Regulatory elements and transcriptional regulation by testosterone and retinoic acid of the rat nerve growth factor receptor promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                   or send
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                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                       SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE I SUBCELLULAR LOCATION: Type I membrane protein. PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED SIMILARITY: CONTAINS 4 THER-CYS REPEATS. SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                     FUNCTION: LOW AFFINITY RECEPTOR WHICH (
AND NT-4. CAN MEDIATE CELL SURVIVAL AS
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                                                                                                      European
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                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                       non-profit
                                                equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                         Bioinformatics Institute. The profit institutions as long
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er and molecular
 : -; NOT_ANNOTATED_CDS
A26431.
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CELL DEATH OF
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Best Local :
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TNR6_PIG
077736;
15-JUL-1999
15-JUL-1999
16-OCT-2001
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PROSITE; PS50052; TNFR_NGFR_2; 4.

PROSITE; PS50017; DEATH_DOMAIN; 1.

PROSITE; PS50017; DEATH_DOMAIN; 1.

Receptor; Neurogenesis; Transmembrane; Glycoprotein;

Receptor; Neurogenesis; Apoptosis; 3D-structure.
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Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
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(Rel. 38, Created)
(Rel. 38, Last sequence (Rel. 40, Last annotation)
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Conservative 3
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TNER-CYS 3.
TNER-CYS 4.
DEATH.
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BY SIMILARITY.
BY SIMILA
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CYTOPLASMIC
TNFR-CYS 1.
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82 40

TKRESECPE----GQHREGQFCCQPCPPGKRKHADCTSPGGAPQCVPCSEGEDYTDKNHH

95

EPSCFPCTVCKSDQKH----KSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQ 137

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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERLPHERAL TOLERANCE, IN THE ANTICEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
-!- SIMILARITY: CONTAINS 3 TMFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                PROSITE; PS00652; TNFR_NGFR_1; 2. PROSITE; PS50050; TNFR_NGFR_2; 2. PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                    Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Expression of apoptosis-associated myocardium of pig.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Bartling B., Hoffmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                             SEQUENCE
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                        Apoptosis;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000488;
InterPro; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ001202; CAP
HSSP; P25445; 1DDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CD95).
TNFRSF6 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
  28
  TARQEEVPOOTVAPQOORHSFKGEECPAGSHR----SEHTGA--CNPCTEGVDYTNASNN
                             44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APT1 OR
                                                                                            116
332 AA;
                                                                                                                                                                                                                                                                     Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Pig)
                             14.0%; ilarity 32.4%; Conservative 2
                                                                                                                      17
176
193
45
82
126
126
227
                                                                                                                                                                                                                                                                                                                                                                                                                  CAA04596.1;
                                                                                                                      175
192
332
81
125
164
311
                                                                                                                                                                                                                                         16 POTENTIAL.
332 TUMOR NECI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                             37592
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                                                                                                                                                                                                                                                                                                                                                                        TNFR_c6
                                                                                                                                                                                                                                                                                                                                                                                          Death
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                                                                                             MW.
                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                             Score 194; DB 1;
Pred. No. 1.4e-05;
4; Mismatches 50;
                                                                                                                                                            TNFR-CYS
                                                                                            N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
; 5B8B03682756BflB CRC6
                                                                                                                                   DEATH.
                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                               SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                 TNFR-CYS
                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                     Transmembrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schulz
                                                                                                                                                  ω N L
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R., Heusch G.,
in hibernating
                                                    Length 332;
                                                                                             CRC64;
                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Sus.
                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Darmer and stun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CASCADE
                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                armer D.;
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                             Gaps
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TRIAL
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PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Receptor; Transmembrane; Glycoproteisional 21 POTENTI CHAIN 22 461 EXTRACE TRANSMEM 211 233 POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning or receptor."
                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH HINTATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

-I- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THEFI LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFES, RIP AND POSSIBLY FADD, ARE RECRUITED TO THEFI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND ME-KAPPA B SIGNALING (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                            EMBL; U19994; AAC48499.1; -. HSSP; P19438; 1TNR. InterPro; IPR000488; Death. InterPro; IPR001368; TNFR_C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96011645;
Suter B., Pauli U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                         ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (p55)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor necrosis
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                     1; PF00531; death; 1.
1; PF00020; TNFR_C6; 3.
20m; PD000771; TNFR_C6; 1.
2T; SM00005; DEATH; 1.
2T; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NCTPTSNTKCREVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163:263-266(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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34,
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.H.;
                                                                                                                                                                                                                                                                                                                            TNFR_c6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                   Glycoprotein; Repeat; Signal; Apoptos POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR 1.
     EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                     Repeat; Signal; Apoptosis.
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Best Local
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DOMAIN
DISULFID
CARBOHYD
CARBOHYD
                                            Mammalia;
Bovidae; B
                                                                            Bos taurus
Eukaryota;
                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
16-OCT-2001 (Rel. 40, Last and
Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
                                                                                                            TNFRSF6 OR APT1 OR
                                                                                                                                                                                                                             TNR6_BOVIN P51867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                           receptor) (Apoptosis-mediating
                                                                                                                               (CD95)
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                                                                                                                                                                                                                                                                                                                                                           SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQQRHSFKGEECPAG--SHRSEHTGACNPCTEGV---
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                                                                                                                                                                                                                                                                                                                                                                                                                             -TPAPAAEETMTTSP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENHLTQCLSCSKCRSEMSQVEISPCTVDRDTVCGCRKNQYRKYWSETLFQCLNCSLCPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
69; Conserv
                                                                                                                                                                                                                                                                                                                              334
                                            ; Eutheria; Cetartiodactyla; Bovinae; Bos.
                                                                            Metazoa; Chordata;
                                                                                             (Bovine).
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                                                                                                                                                                             annotation
                                                                                                                                                                                            sequence
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DEATH.
BY SIMILARITY.
BY S
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TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 188.5; DB Pred. No. 4e-05;
                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             -GTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPA
                                                                                                                                             surface antigen
                                                                                                                                                            superfamily member
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                                                              Ruminantia;
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                                                                                                                                             FAS)
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                                                             Pecora;
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                                                                                                                                           precursor (FASL (Apo-1 antigen)
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                                                              Bovoidea;
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                                                                  5_CHICK
TR16_CHICK
P18519;
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Pfam; PF00031; death; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR, 3.
SMART; SM00208; TNFR, NGFR_1; 2.
PROSITE; PS00652; TNFR_NGFR_2; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
                  01-NOV-1990
01-NOV-1990
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                      REPEAT
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96226401; pubMed=8634151;
YOO J., Stone R.T., Beattie C.W.;
"Cloning and characterization of the bovine Fas.";
DNA Cell Biol. 15:227-234(1996).
-I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                          109
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SUBCELLULAR LOCATION: Type I membrane protein.

DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FAD AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ween the Swiss Institute of Bioinforms 
European Bioinformatics Institute. The 
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
                                                                                                                                                                                                                                 QRHSFKGEECPAGSH-----RSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                       GLEVEQUCTRTRNTKCRCKSNFFCNSSPCEHCNPCTTCEHGIIE--KCTPTSNTKC
                                                                                                                                                                                   ----KSSCIMTRDIVCQCKEGIFRNENSPEMCRKCSRCPSGEVQVSNCISWDDIQC 149
                                                                                                                                                                                                                 REHQFCCQPCPPGKRKNGDCKRDGDTPECVLCSEGNEYTDKSHHSDKCIRCSIC--DEEH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P25445;
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                                                                                                                                                                                                                                                                             l Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001368; TNFR_c6.
      (Rel. 16,
(Rel. 16,
(Rel. 40,
sis factor
                                                                                                                                                                                                                                                                             Conservative
                                                                                  STANDARD;
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36445
                                                                                                                                                                                                                                                                                          13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Death.
Last sequence update)
Last annotation update)
receptor superfamily member 16 precursor (Low-
                                                Created)
                                                                                                                                                                                                                                                                                                                                                        MW.
                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 6. EXTRACELLULAR (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL). TNER-CYS 1. TNER-CYS 2.
                                                                                                                                                                                                                                                                                            Score 187;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                    TNFR-CYS 3.
DEATH.
pt 4D88A90E9E1F4892 CRC64;
                                                                                                                                                                                                                                                                             Mismatches
                                                                                416
                                                                                                                                                                                                                                                                                          DB 1;
.6e-05;
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                                                                                                                                                                                                                                                                                                        Length 323;
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REPEAT
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Pfam; PF00020; TNFR_C6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
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PIR; A60504; A60504.
HSSP; P07174; INGR.
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-I- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMA:
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE
-I- SIMILARITY: CONTAINS 4 TWER-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90152140; PubMed-2154393;
Heuer J.G., Fatemie-Nainie S., Wheeler E.F.,
"Structure and developmental expression of to
Dev. Biol, 137:287-304(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90166579; PubMed=2560385;
Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
Shooter E.M., Reichardt L.F.;
"Structure and developmental expression of the nerve growth factor receptor in the chicken central nervous system.";
Neuron 2:1123-1134(1989).
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Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation; SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50050; TNFR_NGFR_2; ; PROSITE; PS50017; DEATH_DOMAIN;
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         Signal;
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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SER/THR-RICH.
BY SIMILARITY.
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TNFR-CYS
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CYTOPLASMIC (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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he chicken NG
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                                                                                                    RL SUBMITTED (FEB-1997) to the EMBL/GenBank/DDBJ databases.

C-1- FUNCTION: RECEPTOR FOR TWE-ALPHA. THE ADAPTOR MOLECULE FADD RECEPTOR. THE RESULTING RECEPTOR. TRE RESULTING RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYTIC ACTYVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTA-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

C-1- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF TNERL LEADS TO DEATH DOMAIN OF TRADE THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAPS, RIP AND POSSTBLY FADD, ARE RECUTTED TO THERE CASPASE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND CONFIRM BRIGHTON. TYPE I MEMBERADE THIS COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX OF THE SUBCELLULAR LOCATION: TYPE I MEMBERADE PROTESIS AND CONFIRM BRIGHTON. TYPE I SUBCELLULAR LOCATION: TYPE I SUBCELULAR LOCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRIA_BOVIN
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SEQUENCE
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restriction use by non-profit institute.
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Lee E.-K., Talyor M.J., Ke
"Cloning of cDNA encoding
(TNF-RI).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (p55)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
Bovidae; Bovinae; B
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Eukaryota; Metazoa;
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l Similarity 23.4%;
69; Conservative
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receptor 1 precursor (p60) (TNF-R1) (TNF-RI)
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ng bovine tumor necrosis factor-receptor
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Pred. No. 6.4e-05;
6; Mismatches 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00531; death; 1. Pfam; PF00020; TNFR_c6; 3. ProDom; PD000771; TNFR_c6;
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SMART; SM00208; TNFR; 3.
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InterPro; IPR001368;
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                                                                                                                                                                                                                                                        CQCKEGTFRN--ENSPEMCRKCSRCPSGEVQV--
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                                                                       IICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYISCDRSNFGAVASPS
                                                                                                                                                                                                                                                                                                                                                                                                                                     h 12.4%;
Similarity 21.1%;
75; Conservative (
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                                                                                                   -NATVETPAAEETMNTSPG--
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TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 171.5; DB 1
Pred. No. 0.00044;
2; Mismatches 118
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DEATH.
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TNFR-CYS 1.
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5243EF514DFE81C4 CRC64;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                 -CVEEFGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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(POTENTIAL).
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     -CTPV
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RESCUENCE RESCUE
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SEQUENCE FROM N.A.

MEDLINE-91045991; PubMed-2172983;

KOhno T., Brewer M.T., Baker S.L., Schwartz P.E., King !

KOhno T., Squires C.H., Thompson R.C., Vannice J.L.;

"A second tumor necrosis factor receptor gene product of the continuous necrosis factor inhibitor.";

"A second tumor necrosis factor inhibitor.";

"A second tumor necrosis factor inhibitor.";
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TR1B_HUMAN
P20333;
01-FEB-1991
01-AUG-1991
16-OCT-2001
                                                         MEDLINE=93016040; F
Pennica D., Lam V.T
Lipari M.T., Goedde
"Biochemical proper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A receptor cellular and Science 248: [2]
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SEQUENCE FROM N.A.
MEDLINE-90260639; PubMed=2160731;
Smith C.A., Davis T., Anderson D., Solioner S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor cellular and viral proteins.";
Science 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ul-Aug-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor binding protein 2) (TBPII) (p80) (TNF-R2) (p75) (CD120B) (Etanercept).
TNFRSFIB OR TNFR2 OR TNFBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomics [4]
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Lepaslier D., Stallard
Brodeur G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (3)
SEQUENCE FROM N.A.
MEDLINE=96299745; PubM
                          Characterization of ligand phosphorylation.":
                                                                                                                                                                                                                                                                                                                                                                           urine.
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                  phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complementary DNA cloning and demonstration of a sheeproc. Natl. Acad. Sci. U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                distinct
                                                                                                                                                                                                                    *Purification and
                                                                                                                                                                                                                                      Brockhaus M.;
                                                                                                                                                                                                                                                       Loetscher H.,
                                                                                                                                                                                                                                                                           SEQUENCE OF 23-40; MEDLINE=91056048; 1
                                                                                                                                                                                                                                                                                                                                                         tumor necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heller R.A.,
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                                                                                                                                                                                                                                                                                                                                        Biol.
                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis factor-binding
                                                                                                                                                                                                                                                                                                                                  Evidence for immunological cross-reactivity necrosis factor receptors.";
1. Chem. 265:1531-1536(1990).
                                                                                                                                                                             Chem.
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35:94-100(1996).
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49572; PubMed=2166946;
                                                       Goeddel D.V.;
properties of
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                                                                                                                                                                                                                                                     3-40; 65-69; 136-141;
048; PubMed=2173696;
Schlaeger E.J., Lahm
                                                                                                                                                                                                                                                                                                                                                                                                                215; PubMed=2153136;
Novick D., Wallach
                                                                                                                                                                           necrosis factor receptors 265:20131-20138(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PubMed=8661109;
White P.S., Maris
allard B.J., Goedd
                                                                                             PubMed=1328224;
.T., Mize N.K.,
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.A. 87:6151-6155(1990).
                                  the 75-kDa tumor necrosis binding, internalization,
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Goeddel D.V
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tors from HL60 cells.";
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.V., Desauvage
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F.J.,
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Park Y.C., Burkit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to servere rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an Immuglobulin Fc chain. It binds to TNF-alpha and blocks its interactions with receptors. SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
DATABASE: NAME-PROW; NOTE-CD guide CD120b entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
DATABASE: NAME-Enbrel; NOTE-Clinical information on Enbrel; WWW-"http://www.enbrelinfo.com/".
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PS50050;
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Transmembrane; Glycoprotein;
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t V., Villa A.R.,
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Matches 74
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P15725;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily mer
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                                                                                                                                                                                                                                                                           mallett S., Fossum S., Barclay A.N.; "Characterization of the MRC OX40 antigen of activated CD4 positive '"Characterization of the MRC OX40 antigen of activated CD4 positive 'Iymphocytes -- a molecule related to nerve growth factor receptor."; EMBO J. 9:1063-1068(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor) (OX40 antigen) (TNFRSF4 OR TXGP1L OR OX40. Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                            MEDLINE-90214614; PubMed-2157591;
Mallett S., Fossum S., Barclay A.
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane pro-
TISSUE SPECIFICITY: ACTIVATED T-CELLS.
SIMILARITY: CONTAINS 4 THER-CYS REPEATS.
                                                                                                                                                                                                                                                      FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPAPA-AEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPEPSTAPSTSFLLPMGPSPPAEGS-TGDFALPVG-----LIVGVTALGLLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVFCTKTSDT-VCDSC-EDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNRICTCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTTSSTDICRPHQICNVVAIPGNASRDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGTFRNENSPEMCRKCS---RCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 25.74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSEHTGACNPCTEGVDYTNASNNEPSCFPC-TVCKSDQKHKSSCTMTRDTVCQCK 112
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118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPAAEETMNTS-----PGT---PAPAAEETMTTSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.
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BY SIM
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603B580ECD67636F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169.5;
No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 1;
                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KPCAPGTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor (0X401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus
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TNR4_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 63
                                                                                                                                             HUMAN
TNR4_HUMAN
TNR4_HUMAN
P43889; Q13663;
Ol-NOV-1995 (Rel. 32, Created)
Ol-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-granecrosis factor receptor superfamily member 4 / TAX-transcriptionally act
               SEQUENCE FROM N.A.

MEDLINE=94170844; PubMed=7510240;
Latza U., Duerkop H., Schnittger S., Ring
Hummel M., Fonatsch C., Stein H.;
"The human OX40 homolog: cDNA structure,
assignment of the ACT35 antigen.";
Eur. J. Immunol. 24:677-683(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
PIR; ;
PIR; ;
SEQUENCE
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00020; TNFR_c6; 3. ProDom; PD000771; TNFR_c6; SMART; SM00208; TNFR; 3.
                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                         218
                                                                                                                                                                                                                                                                                       200
                                                                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                                                                    161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; S08036; S08036.
; S12783; S12783.
P; P19438; TEXT.
                                                                                                                                                                                                                                                                                      STPTLVA-----PEGPAFAVILGLGLGLLAPLTVLLALYL
                                                                                                                                                                                                                                                                                                         GTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
                                                                                                                                                                                                                                                                                                                               GKQIRH----
                                                                                                                                                                                                                                                                                                                                                   TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETM-TTSPGTPAPAAEETMTTS--P
                                                                                                                                                                                                                                                                                                                                                                                                                                     ECPAGS - - - HRSEHT - - GACNPCTEGVDYTNASNNEPSCFPCTVC - - KSDQKHKSSCTMT
                                                                                                                                                                                                                                                                                                                                                                       EDTYCQCRPGTQPRQDSSHKLGVDCVPCPPGHFSPGSNQACKPW
                                                                                                                                                                                                                                                                                                                                                                                           RDTVCQCKEGTF-RNENSPEMCRKCSRCPSGEVQVSN---CTSWDDIQCVEEFGANATVE 160
                                                                                                                                                                                                                                                                                                                                                                                                               ECQPGHGMVSRCDHTRDTVCHPCEPG--FYNEAVNYDTCKQCTQCNHRSGSELKQNCTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X17037; CAA34897.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M00208; TNER, ...
PS00652; TNER_NGER_1; 3.
; PS50050; TNER_NGER_2; 2.
; PS50050; Antigen; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
211
236
25
61
103
124
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                                                                                                                                                                                                                                                                                                                               PASNSLDTVCEDRSLLATLLWETQRTTFRPTTVPSTTVWPRTSQLP
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235
271
60
102
123
164
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271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 4.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TMER-CYS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR-CYS
TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL); C06465136B16EB21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 0.0
                                                           Ringeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                      expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                 Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
                                                           J.,
                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                     activated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                             Eitelbach
                                       and
                                                                                                                            Euteleostomi;
                                                                                                                                                                             precursor (0X40L
                                       chromosomai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271;
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RESULT
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ID TN
AC P4
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Best Local S
Matches 59
_MOUSE
TNR4_MOUSE
P47741;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  its activities on OX40 receptor.";

Circ. Shock 44:30-34(1994).

-:- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

-:- SUBCELLULAR LOCATION: Type I membrane protein.

-:- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

-:- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd134.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X75962; CAA53576.1; --
EMBL; S76792; AAB33944.1; ALT_INIT.
HSSP; P25942; 1CDF.
MIM; 600315; --
                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00020; TNFR_C6; 3. ProDom; PD000771; TNFR_C6; 1. SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson "Identification of 0X40 ligand and preliminary characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95219871; PubMed=7704935;
                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                            195
                                                                                                                                               150
                                                                                                                                                                         161
                                                                                                                                                                                                   102
                                                                                                                                                                                                                            104
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                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   ECPAGS-----HRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVC--KSDQKHKSSCTM 103
                                                                                                                                                                      TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTP
                                                                                                                                                                                                                          TRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSN---CTSWDDIQCVEEFGANATVE 160
                                                                                          WPRTSQGPSTRPVEVPGGRAVAAILGLGLVLGLLGPLAILLALYL
                                                                                                                    APAAEETMTTSP-GTPASSHYLSCTIVGIIV-----LIVLLIVFV
                                                                                                                                                                                                   TQDTVCRCRAGT
                                                                                                                                                                                                                                                   ECRPGNGMVSRCSRSQNT-VCRPCGPGF-YNDVVSSKP-CKPCTWCNLRSGSERKQLCTA 101
                                                                                                                                               AGKHTLQ----
                                                                                                                                                                                                                                                                                                       Similarity 26.: 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                       29
215
236
30
66
108
127
146
160
277
    (Rel.
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29
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                            STANDARD;
                                                                                                                                                                                                  -QPLDSYKPGVDCAPCPPGHFSPGDNQACKPW-----
    33,
                                                                                                                                               -PASNSSDAICEDRDPPATQPQETQ----GPPA----RPITVQPTEA
                                                                                                                                                                                                                                                                                                                                                                                                 214
235
277
277
107
126
167
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277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                       29340
                                                                                                                                                                                                                                                                                                                     26
    Created)
                                                                                                                                                                                                                                                                                                                  . 28;
                                                                                                                                                                                                                                                                                                                                                                         Œ.
                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 3 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                      Score 166.5;
Pred. No. 0.00
%6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
49F15525941550BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             TNFR-CYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NECROSIS
                            272
                                                                                                                                                                                                                                                                                             ; DB 1,
0.00055;
83;
                                                                                                                                                                                                                                                                                                                                                                                                                        (INCOMPLETE).
                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                Length
                                                                                           239
                                                                                                                                                                                                -TNCTL-
                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.R.;
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                149
                                                                                                                                                                        220
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밁
                     QY
                                            Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of rat OX40 protein.";
Eur. J. Immunol. 25:926-930(1995).
-i- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SUBCELLULAR CONTAINS 4 TNFR-CYS REPEATS.
                                                                                                   REPEAT
REPEAT
REPEAT
REPEAT
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                 DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94044750; PubMed-8228223;
Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
Claassen E., Noelle R.J., Fell H.;
"Claassen E., Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate
T-B cell interactions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor)
                                                                                                                                                                                                                                                                                                 ProDom; PD000771; TNFR_c6; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                        EMBL; Z21674; CAA79772.1; -. EMBL; X85214; CAA59476.1; -. HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as modified and this statement is not removed. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birkeland M.L., Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95255413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-B cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFRSF4 OR TXGP1 OR OX40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor necrosis factor receptor superfamily member 4
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                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                       InterPro; IPRO01368; TNFR_c6. Pfam; PF00020; TNFR_c6; 3.
                                                                                                                                                                                                                                                                                                                                               MGD;
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                                                                                                                                                                                                                                                                           PROSITE;
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    Immunol.

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MGI:104512; Tn
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                     AVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKG----EECPAGS---HRSEHT--GA
ALLLALTLGVTARRLNCV----
                                             67; Conser
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Copeland N.G., Gilbert D.J.,
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TNFR_NGFR_2; 2.
Antigen; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNER-CYS 1.
TNER-CYS 2.
TNER-CYS 2.
                                                                                                     ₹,
                                            37;
                                            Score 166; DB
Pred. No. 0.00
37; Mismatches
                                                                                                              A ->
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TNFR-CYS 4
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                                                                                                    -> G (IN REF. 2).
06E7BB4156F0D08E CRC64;
 ---KHTYPSGHKCCRECQPGHGMVSRCDHTRDTL
                                                     166;
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                                             106;
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Maximum Match 100%
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Maximum DB
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3: sp_fungi:*
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5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organeli:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_rodent:
12: sp_virus:*
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14: sp_unclass
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15: sp_archeap
17: sp_archeap
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Gapop 10.0 , Gapext 0.5
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1382
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Copyright (c) 1993 - 2000 Compugen
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09jjl5 mus musculu
05jl15 mus musculu
057408 meleagris g
09iar7 gallus gall
09pw79 gallus gall
09pw79 gallus gall
0920w1 mus musculu
09prg7 xenopus lae
09cra4 mus musculu
09prg62 mus musculu
09prg64 oryctolagus
09df34 brachydanio
023635 caenorhabdi
                                                                                                                                                                       Q96e62 homo sapien
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	10.	10.7	•	10.8	•	10.9	•	11.1	11.2	11.6	11.7	11.7	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.9	11.9	11.9	11.9	11.9	٠	11.9	•	12.7
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Ovo/11 min strong	Q99K36 macaca assa	Q9nax4 dictyosteli	097530 canis famil	homo s	feli	Q92954 homo sapien		ד	xen	Q9er63 mus musculu	075509 homo sapien	Q9g140 macaca mula	Q9bdp0 aotus trivi		Q9bdn0 macaca neme	Q9bdn4 cercocebus	Q9tsn4 macaca fasc	Q9dcq1 mus musculu	Q9gk28 macaca arct	mus	Q91xh9 mus musculu	mus			Q9tv79 oryctolagus	Q9xs60 oryctolagus	Q16042 homo sapien	097491 ovis aries

## ALIGNMENTS

Qy 123 EMCRKCSR-CPSGEVQVSNCTSWDDIQCVEEFGAN 156	Оу 63 т рь 142 р	Qy 3 R     Db 87 R	Query Match Best Local : Matches 9		_	<pre>RL Submit DR EMBL;</pre>			RP SECUEN		OC Mammal				_	-	AC Q96E62;		Q96E62
	TGACNPCTEGVDYTNASNNEDSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSP 122                                : :	RIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQORHSFKGEECPAGSHRSEH 62 	Query Match 35.2%; Score 486; DB 4; Length 468; Best Local Similarity 60.0%; Pred. No. 1.9e-32; Matches 93; Conservative 16; Mismatches 40; Indels 6; Gaps	NCE 468 AA; 50061 MW; 7E9661859A550CD4 CRC64;	tor.	Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC012866; AAH12866.1;	Strausberg R.,	TISSUE-OVARY, AND ADENOCARCINOMA;	SEQUENCE FROM N.A.	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	TUMOR NECROSIS FA	(TrEMBLrel. 19,	C-2001 (TrEMBLrel. 19, Last sequence update)	2001 (Tremaire) 19	PRELIMINARY; PRT; 468 AA.	

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RESULT

Q9JJIL6

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AC Q9

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Best Local S
Matches 58
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Pfam; PF00020; TNFR_C6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1
PROSITE; PS00652; TNFR_NGFR_1; UNI
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                Q9JJL6;
Q9JJL6;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRAIL RECEPTOR KILLER/DR5 HOMOLOGUE.
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090ZM4
01-MAY-2000 (TrEMBLrel 13, Created)
01-MAY-2000 (TrEMBLrel 13, Last sequence
01-DEC-2001 (TrEMBLrel 19, Last annotati.
KILLER/DR5 TRAIL DEATH-INDUCING RECEPTOR.
TNFRSF10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILINE-99310501; PubMed-10383128;

Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.

"Molecular cloning and functional analysis of the mouse h

the KILLER/DR5 tumor necrosis factor-related apoptosis-in

(TRAIL) death receptor.";

Cancer Res. 59:2770-2775(1999).
Nakamura Y.,
"Mouse TRAIL
                                               TISSUE-SPLEEN;
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                       TNFRSF10B OR MK.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF176833; AAD52656.1; HSSP; 014763; 1D0G.
                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
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                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                     Tamari
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                                                                                                                                  Chordata;
Rodentia;
         ] <u>*</u>
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                       Watanabe
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Pred. No. 5.
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Sciurognathi; Muridae;
                                                                                                                                  Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                  Euteleostomi;
; Murinae; Mus
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Best Local S
Matches 56
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Best Local S
Matches 57
                                                                                                                          InterPro; IPR000488; Death.
InterPro; IPR001588; TNRR_C6.
Pfam; PF00020; TNFR_C6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1
PROSITE; PS50652; TNFR_NGFR_1; UN
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                   Q9JJL5;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
TRAIL RECEPTOR2 KILLER/DR5;
                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Wat. Nakamura Y., Tamari M., Wat. "Mouse TRAIL receptor genom Submitted (AUG-1999) to the EMBL; AB031082; BAA96463.1;
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00020; TNFR_c6; 2
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
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PROSITE; PS00652;
PROSITE; PS50050;
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InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6
                                                                                                                                                                                                                            HSSP; 014763; 1D0G
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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HSSP; O14763; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1999) to the EMBL; AB031081; BAA96462.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 VVVIVAVLLPVLAYSATT-----ARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGA 65
             VVVIVAVLLPVLAYSATT-----ARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGA
LAMLQAVFVPVTANPAHNRPAGLQRPEESPSR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKPCREGIDYTSHSNHSLDSCILCTVCKEDKVVETRCNITTNTVCRCKPGTFEDKDSPEI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQSCSNCTDGEEELTSCTPRENRKCVSK
                                            ch 20.18;
Similarity 37.88;
56; Conservative 2
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; TNFR_NGFR_1; U
; TNFR_NGFR_2; 2
                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
                                                                                                      42676 MW;
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to the EMBL/
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                                            Score 277.5; DB 11
Pred. No. 2.6e-15;
3; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 282.5; DB 11;
Pred. No. 9.8e-16;
B; Mismatches 42;
                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                             UNKNOWN_1.
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                                                                                                      4FD089FCDA134159 CRC64;
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annotation updat
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Pfam; PF00531; death; 1.

Pfam; PF00020; TNFR_C6; 2.

SMART; SM00005; DEATH; 1.

SMART; SM00005; TNFF; 2.

PROSITE; PS00198; 4FE45_FERREDOXIN; UNKNOWN_1.

PROSITE; PS50017; DEATH_DOMAIN; 1.

PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.

PROSITE; PS009652; TNFR_NGFR_1; UNKNOWN_2.

PROSITE; PS50050; TNFR_NGFR_2; 2.
   Q9IAR7;
01-OCT-2000
01-OCT-2000
01-DEC-2001
TVBS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O57408 PRELIMINARY; PRT; 368 AA.
O57408;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SUBGROUP E ALV RECEPTOR.
Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor.
SEQUENCE
                                                                                       Q9IAR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000488; Death.
InterPro; IPR001865; Ribosomal_S2
InterPro; IPR001368; TNFR_c6.
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MEDLINE=97471016; Pubme
Ackins H.B., Brojatsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001450; 4Fe4S_ferredoxin.
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EMBL; AF006002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a cellular receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9103;
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                                                                                                                                                                                                                                                                                                                                                  LKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQSCSNCTDGEEELTSCTPRENRKCVSK 172
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                                                                                                                                                                                                                                              PCKKD-EYTEYPNDFPKCLGCRTCREDQVEVSPCNSTRNTRCACKNGTFCLPDHPCEMCQ
                                                                                                                                                                                                                                                                                                                  LRFCPVLLLLLAKVHLGSAAAVKKRAVKSDVLKPDPY----SKKCPMGTYLANDSSRCL
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                   (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                         PRELIMINARY;
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AAB93987.1; -
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atsch J., Naughton J.,
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34.7%;
                     15,
15,
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                   Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                   Score 253; DB 13;
Pred. No. 2.6e-13;
7; Mismatches 59
                                                                                                                                                                                                            149
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                                                                                           PRT;
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InterPro; IPRO00488; Death.
InterPro; IPRO0138; TMFR_C6.
IPFO0511; Geath; 1.
IPFO0512; Geath; 1.
IPFO0020; TMFR_C6; 2.
SWART; SM002005; DEATH; 1.
IPFO017E; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
IPROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
IPROSITE; PS0017; DEATH_DOWALN; 1.
IPROSITE; PS00052; TMFR_NGFR_2; 2.
IPROSITE; PS00055; TMFR_NGFR_2; 2.
IPROSITE; PS00050; 
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01-MAY-2000
01-MAY-2000
01-DEC-2001
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J. Virol. 74:3572-3578(2000).
J. EMBL, AF161713; AAF60221.1; -...
                                                                                                                                                                                       Brojatsch J., Naughton J., Rolls M.M., Zingler K., You "CARI, a TNFR-related protein, is a cellular receptor avian leukosis-sarcoma viruses and mediates apoptosis. Cell 87:845-855(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukarvota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=20193796; PubMed=10729132;
MEDLINE=20193796; PubMed=10729132;
MEDLINE=20193796; PubMed=10729132;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
SEQUENCE FROM N.A. Brojatsch J., Naughton J., Naughton J., Submitted (JUN-1999) to the EMBL; AF161712; AAD47256.1;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=97100985; PubMed=8945512;
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KC-SRCPSGEVQVSNCTSWDDIQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCKKD-EYTEYPNDFPKCLGCRTCREDQVEVSPCIPTRNTQCACKNGTFCLPDHPCEMCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSP-EMCR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRLCPVLLLLFAEVQLGSAAAVKKRADRSDLQKPDLYR----RKCPMGTYEANDSIQCL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCQTECPKGQVRLAPCTQHSDLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13,
19,
                                       Young J.A.T.;
e EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 222;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0553CE531DEB47C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                              .A.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                            Young
                                                                                                                                                                                                                                      . ";
                                                                                                                                                                                                                                                                                                            J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phasianinae;
                                                                                                                                                                                                                                                                 cytopathic
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Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO01450; 4Fe4S_ferredoxin.

InterPro; IPRO0148B; Death.

InterPro; IPRO0136B; TNFR_C6.

InterPro; IPRO0136B; TNFR_C6.

Pfam; PF00531; death; 1.

Pfam; PF00531; death; 1.

Pfam; PF00020; TNFR_C6; 2.

SMART; SM002005; DEATH; 1.

SMART; SM002005; TNFR_C6; 2.

PROSITE; PS0019B; 4FE4S_FERREDOXIN; UNKNOWN_1.

PROSITE; PS0019B; 4FE4S_FERREDOXIN; UNKNOWN_1.

PROSITE; PS00501; DEATH_DOMAIN; II.

PROSITE; PS00502; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS0050; TNFR_NGFR_2; 2.

SEQUENCE 368 AA; 41515 MW; F558C225AB3750BB CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                Pfam; PF00031; death; 1.

Pfam; PF00030; TNFR_C6; 3.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 3.

SMART; SM00208; TNFR; 3.

PROSITE; PS00109; CYPOCHROME_C; UI

PROSITE; PS50017; DEATH_DOMAIN; 1

PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                         Q9DFV0;
Q9DFV0;
Q1-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                       "Molecular cloning and expression of a TNF ligands in the fish ovary."; Comp. Biochem. Physiol. B. (Comp. Biochem. 1 EMBL; AF250042; AAG24365.1; -...
                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (zebrafish) (Zebra danio),
Eukaryota; Metazoa; Chordata; Craniata; Vert
Actinopterygii; Neopterygii; Teleostei; Eute
Cypriniformes; Cyprinidae; Danio.
                                                              SEQUENCE
                                                                                                                                                                      InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                              ZFIN; ZDB-GENE-010802-1; tnfrsfa.
                                                                                                                                                                                                                                                                                     Bobe
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                       TNFRSFA
                                                                                                                                                                                                 InterPro; IPR000345; CytC_heme_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCQTECPKGQVRLAPCTQHSDLLC
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  Similarity 51; Conserv
                                                                                                                                                                                                                                                                                     Goetz F.W.;
                                                              438
                                                                                                                                                                                                                                                                                                                                                                                                         1 (TrEMBLrel. 16,
1 (TrEMBLrel. 16,
1 (TrEMBLrel. 19,
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                              A
A
                                                              49103 MW;
            14.9%;
27.6%;
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31.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
  29;
                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
           Score 206; DB 13;
Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 212; DB 13;
Pred. No. 6.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                            B7E5312BE6E80B04 CRC64;
                                                                                                           UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          438
                                                                                                                                                                                                                                                                                                                                              Vertebrata; Euteleostei;
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                                                                                                                                                                                                                                                                       receptor and
 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                        Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
 Indels
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                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                              Ostariophysi;
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24;
                                                                                                                                                                                                                                                                       TNF
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Gaps
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                                                                                                                                                                                                                         Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                       Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_C6; 4.
PRINTS; PR01497; SHALCHANNEL.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
PROSITE; PS50017; DEATH_DOMAIN; 1
PROSITE; PS500652; TNFR_NGFR_1; UN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TIEMBLIGEL 17, C
01-OCT-2001 (TIEMBLIGEL 18, L
01-DEC-2001 (TIEMBLIGEL 19, L
DEATH RECEPTOR 6.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                    PROSITE;
Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bridgham J.T., Johnson A.L.;

"Expression of DR6 in the ove

Submitted (MAY-201) to the

EMBL; AF349908; AAK29666.2;

HSSP; P19438; INCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q98SM6;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000488; Death.
InterPro; IPR003975; Shal_channel
InterPro; IPR003368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                           179
                                                                                                   117
   203
                                                  154
                                                                          124
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                                                                                                                          65
                                                                                                                                                                                      14 IVAVLLPVLAYSATTARQEEVPQQTVA------PQQQRHSFKGEECPAGSHRSEH
                                                                                                                                                  63
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                                             GANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSP----
                                                                        QINDTCVPYTVCPVGWGVRKKGTETEDVRCKPCLRGTFSDVPSSVMKCKTYTD-
                                                                                                                                                                       VLAAVLPELVFLGTADAQPKLTSEQNAVSLPAGKYLHLDRATNQELICDKCPAGTYVSKH
                        GKNMVVVKPGTKESDNVC-GSPASLPNTSLTSS----DAQADGETYEAPPTAYLPKGLNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTKSTLRECSPCPDGT-FTKHENGIERCHPCRKPCELPMIEKTHCTALTDRECTCLSGTF
                                                                                                                                                -----TGACNPCTEGVDYTNASNNEPSCFPC-TVCKSDQKHKSSCTMTRDTVCQCKEGTF 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETMNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQCKEGTFRNENSP-EMCRKCSRCPSGEVQVSNCTSWDDIQCVE--EFGANATVETPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGSHRSEH-----TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt AGTYVKEKCTSGHVMGKCSPCEKGT-YAEHPTGMEQCLQCSQCHRDQTVVAECTSTSNTK}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAMKVCMALVIFSLALVGHGAAELGVSADHQNRTARQMTCLENHEYP---HNGFCCKNCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTLKFVVVIVAVLLPVLAYSAT------TARQEEVPQQTVAPQQQRHSFKGEECP
                                                                                                                                                                                                                          Similarity
69; Conserv
  GTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
                                                                                                                                                                                                                                                                                       651 AA;
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                            TNFR_NGFR_2;
                                                                                                                                                                                                                                                                                       71003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                    14.48; 24.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovary.";
he EMBL/GenBank/DDBJ
                                                                                                - NENSPEMCRKCSRCPSGEV - - QVSNCTSWDDIQCVEEF
                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                    Score 199; DB 13; Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                     BDC95A600DAB2C2A CRC64;
                                                                                                                                                                                                                                                                                                                        UNKNOWN_1
                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                          109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                                Length 651;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phasianinae;
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                                                                          -C---F
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Pfam; PP00531; death; 1.

Pfam; PP00020; TNFR_C6; 4.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 3.

PROSITE; PS50017; DEATH_DOMAIN; 1.

PROSITE; PS01186; EGF_2; UNKNOWN 1.

PROSITE; PS0120; LIPASE_SER; UNKNOWN_1.

PROSITE; PS00652; TNFR_NGFR_1; 3.

PROSITE; PS50050; TNFR_NGFR_2; 4.
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Q9Z0W1;
01-MAY-1999
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HSSP; P07174; INGR.
MGD; MGI-97323; Ngfr.
InterPro; IPR000488; Death.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
     Q9PRG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000734; Lipase.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "LOW-affinity nerve-growth factor receptor receptor for rabies virus.";

EMBO J. 17:7250-7259(1998).

EMBL; AF105292; AAN17047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99077793; PubMed=9857182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                        146
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                                                                                                                                                                                                                                        CSVCGVGSGLVFSCQDKQNTVCEECPEGTYSDEANHVDPCLPCTVCEDTERQLRECTPWA
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                                                                                               QP-----VVTRGT---
                                                                                                                                                                   DAECEEIPGRWITRSTP-PEGSDVTTPSTQEPEAPPERDLIASTVA----DTVTTVMGSS
                                                                                                                                                                                                    DIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTP
                                                                                                                                                                                                                                                                                                                EPCLDSVTFSDVVSATEPCKPCTECLGLQSMSAPCVEADDAVCRCSYGYYQDEETGRCEA
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     PRELIMINARY;
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                                                                                               -ADNLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
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Pred. No. 9.2e
35; Mismatches
                                                                                                                                                                                                                                                                 -QCKEGTFRNE-NSPEMCRKCSRCPSGEVQVSNCTSWD
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     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5D7A4510DB8AF9B2 CRC64;
                                                                                             PVYCSILAAVVVGLVAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D., Kieffer B., Flamand A.; receptor (P75NTR) can serve
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                                                                                             263
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Q9CZA4
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Best Local S
Matches 58
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Pfam; PF00020; TNFR_C6; 4.
SMART; SM00005; DEATH, 1.
SMART; SM00208; TNFF; 4.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1
PROSITE; PS0152; TNFR_NGFR_1; UNKNOWN_SPROSITE; PS00505; TNFR_NGFR_2; 3.
                                                                                                                                                                             Q9CZA4 PRELIMINARY;
Q9CZA4;
Q9CZA4;
Q1_JUN-2001 (TrEMBLrel. 17,
Q1_JUN-2001 (TrEMBLrel. 17,
Q1_DEC_2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor.
SEQUENCE
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"Life and death in the developing Xenopus retineurotrophin receptor.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ EMBL; AF172400; AAD51031.1;
EMBL; AF172399; AAD51030.1;
HSSP; P07174; INGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
P75 NEUROTROPHIN RECEPTOR A-2.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-112178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                           Mus musculus (Mouse).
                                                                                                                                              2810028K06RIK PROTEIN.
TNFRSF1AL2 OR 2810028K06RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000488; Death.
InterPro; IPR000561; EGF-like.
InterPro; IPR001368; TNFR_c6.
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                                                                                                                                                                                                                                                                                                                                                       GTSVPPFDLSSSSATTSGDSKVLPPTGVAENLI-----PVYCSILAAVIAGLVAFIV
                                                                                                                                                                                                                                                                                                                                                                               GTPAP---AAEETMTTSPGT----PAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIV
                                                                                                                                                                                                                                                                                                                                                                                                                           CPEGTYSDEDNDRDPCLPCTICEDGEIEAKECTFTSDTVCYDPNPRVSSVTPASSDFPYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVETPAAEETMNTSPGTPAPAAEE-----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAPCVESDDAVCACAYGYFTDKKSGQ-CKLCKSCPEGFGMMMSCTNIQDTIC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYTAKGECCISCQVGEGVIKRCGVNQTVCEPCLDSVTYSDTISHTEACKPCTECFGHKRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58,
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 PubMed=11217851;
                                                                                         Chordata;
Rodentia;
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                                                                                                                                                                                                                     Created)
                                                                                                                                                                                 Last sequence update)
Last annotation updat
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                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                           PRT;
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.5e-08;
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104;

Indels

Gaps

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138 157 85 97

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Length

401; 42;

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Euteleostomi;

Pipidae;

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Euteleostomi; ; Murinae; Mus

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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; Irrovalle, pfam; pr00020; TNFR; 6; 3.

SMART; SM00208; TNFR; 3.

SMART; SM00208; TNFR; 3.

PROSITE; PS00190; CYTOCHROME_C; Ut
PROSITE; PS50050; TNFR_NGFR, 2; 2.
                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TUMOR NECROSIS FACTOR RECEPTOR P60 HOMOLOGUE 2.
TNFRSFIAL2 OR TNERH2.
                                                                                                                                                                                                                                Mus musculus domesticus (western European house mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                              Q9ER62;
                                    MEDLINE=20519229; PubMed=11063728; Engemann S., Stroedicke M., Paulsen Lane N., Reik W., Walter J.; "Sequence and functional comparison implications for a novel imprinting Hum. Mol. Genet. 9:2691-2706(2000).
                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-129 SV;
  SEQUENCE FROM
                                                                                                                                                                                                                  NCBI_TaxID=10092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1930270; Tnfrsf1al2.
InterPro; IPR000345; CytC_heme_bind
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK012838; BAB28502.1; -.
HSSP; P19438; IEXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPLQVKFAMLELHSFK---CPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-FTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PQGIPVLQECNSTANTVC
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 185; 30.4%; Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                     in the Beckwith-Wiedemann region: centre and extended imprinting.";
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                                                                                                              Franck O., Reinhardt
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Fukuda S.,
manaka I.,
Saito R.,
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                                                                                                                  R.,
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Best Local S
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               002764
                                                                                                                                                                                Signal.
                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                               rrouom; PD000771; TNFR_66; 1.
SMART; SM00208; TNFR; 3.
PROSITE; PS00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                              "Expression of OX40 and OX40 ligand genes in rabbit HTL'
T cell lines.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AB003911; BAA20059.1; -.
HSSP; P25942; ICDF.
InterPro; IPR001368; TMFR_c6.
Pfam; PF00020; TMFR_c6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TREMBLrel. 04, 01-JUL-1997 (TREMBLrel. 04, 01-DEC-2001 (TREMBLREL. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1930270; Tnfrsflal2.
InterPro; IPR000345; CytC_heme_bind
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AJ278265; CAC16406.1; . . EMBL; AJ278505; CAC27353.1; - . HSSP; P19438; 1EXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OX40 PRECURSOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CHBB:HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Engemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sono T., Seto A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
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                       Similarity
                                                                                                                                                                                                                          PS00652; TNFR_NGFR_1; PS50050; TNFR_NGFR_2;
                                                                                                    <1
19
267
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267
28489
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31.7%;
                    13.1%;
                                                                                                             MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
Score 181; DB
Pred. No. 1.6e
29; Mismatches
                                                                                                                                    OX40
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Pred. No. 8
                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                               NN
                                                                                                             A8B4CD3173C9500B
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  DB 6; 1
L.6e-07;
mes 81;
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.5e-08;
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                                                                                                             CRC64;
                                         Length 267
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52

65;

Conservative

29;

Indels

46;

Gaps

15;

ECPAG-----SHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVC--KSDQKHKSSCTM 103

E. .

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Q9DF34
ID Q9DF34
AC Q9DF34
AC Q9DF34
AC Q9DF34
DT 01-MAR
DT 01-DEC
DEATHHOUS
CC Eukary
OC Eukary
OC Cyprin
OX NCBI_T
RN [1]
RN [1]
RP SEQUEN
RA Long Q (RT "Stinu
RT "Stinu
RT FECEL
DR HSSP,
DR InterF
DR InterF
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DR Ffam;
DR Pfam;
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                                                                                                                                                                                                                                                                                               Query Match 12.9
Best Local Similarity 25.4
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
SMART; SM00208; TNFR; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9DF34; PRELIMINARY; PRT; 357 AA.

O9DF34; O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEATH RECEPTOR.

Brachydanio rerio (Zebrafish) (Zebra danio).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;

Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;

"Stimulation of erythropoiesis by inhibiting a new hematopoietic receptor in transgenic zebrafish.";

receptor in transgenic zebrafish.";

Nat. Cell Biol. 0:0-0(2000).

EMBL; AF302789; ARG21396.1; -.

EMBL; AF302789; ARG21396.1; -.

HSSP; P19438; IEXT.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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TSTONTRCKCRNGSFCLPDOACEVCKKCSRCKEDEETEKSCTAISNTVC
                               TMTRDTVCQCKEGTF-RNENSPEMCRKCSRCPSGEVQVSNCTSWDDIQC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSTP----TLEASKG-PQLAIVLSLGLGLGLLALLAALL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- NCPAGTYVKKACAAAAEKGVCAPC-EFDTYTEHDHGLLKCISCDKCRIDQETIEKC
                                                                                                                                                FKGEECPAGSH-----RSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSC 101
                                                                                                                                                                                                                                                                                                                                                                                                                           357 AA; 40662 MW; 1652B4840D9EEDBA CRC64;
                                                                                                                                                                                                                                                                                            12.9%; Score 178.5; DB 13; 25.4%; Pred. No. 3.5e-07; Live 31; Mismatches 58;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                   357;
                                                                                                                                                                                                                                                                                                 37;
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	sequence
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## ALIGNMENTS

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                                                   Query Match
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Matches 259; Conserv
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                                                                                                                                                                                                                                                         TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 95,373
REFERENCE/DOCKET NUMBER: PF34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                  TOPOLOGY:
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MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVDQQTVAPQQQRHSFKGEECPAGSHRS 60
                                             100.0%;
nilarity 100.0%;
Conservative 0;
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309-8512
200: 2:
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                                                 Score 1382; DB 4;
Pred. No. 5.3e-102;
D; Mismatches 0;
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                                                                                       Length
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MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRS

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RESULT 3
US-09-086-483A-2
; Sequence 2, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
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; ORGANISM: Human
US-09-153-927-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-153-927-3
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Best Local
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                                                                                                                                                                                                                                                                                                                                      Matches
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LENGTH: 299
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                                                                                                                                                                                                                                                                                                   1 MARIPKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRS 60
                                                                                         EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN 120
                                                                                                                                          ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY
                                                                                                                                                       ETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHY 240
                                                                                                                                                                                                                                      EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN
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o. 6297022
                                                                                                                                                                                                                                                                                                                                               Similarity
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Pred. No. 6.3e-102;
Mismatches 0;
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      RESULT 4
US-09-086-483A-6
; Sequence 6, Application
; Patent No. 6214580
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 132; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICATION NUMBER:
FILING DATE: Dec-9-9
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ADDRESSEE: HUMAN GEN
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                               US/09086483A
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REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              65 ACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/050,936 FILING DATE: May-30-97 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                               35 PKILKFVVFIVAVLLPVRVDSATIPRQDEVPQQTVAPQQQRRSLKEEECPAGSHRSEYTG
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                                                                                       NTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSC 243
                                                                                                                                                           CRKC-SRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETM 183
                                                                                                                                                                                                                                                                                                                                    PKTLKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTG 64
                                                                                                                                   CRTCRTGCPRGMVKVSNCTPRSDIKCKNESAASSTGKTPAAEETVTTILG
                                                                                                                                                                                                                       ACNPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSFQDKNSPEM 154
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9410 KEY WEST AVENUE
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; Pred. No. 9.7e-43;
22; Mismatches 41
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RESULT 5
US-09-013-895A-2
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                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ni, Jian
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                                                       APPLICANT:
TITLE OF IN
                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/050,936
FILING DATE: May-30-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                123 EMCRKCSR-CPSGEVQVSNCTSWDDIQCVEEFGAN 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
TYPE: a
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                              EMCRKCSTGCPRGMVKVKDCTPWSDIECVHKESGN 236
                                                                                                                                                                                                                                                                                                                                                                PGACNRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCKPGTFRNDNSA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
: ROSEL,
: Panes G.
: Panes G.
!: Gentz, Reiner L.
r: Dixit, Vishva M.
INVENTION: Death Domain Containing Receptor 4 (DR4: Death
INVENTION: Receptor 4), Member of the TNF-Receptor
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.2%; Score 472; DB 4; Length 467; 58.7%; Pred. No. 7.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
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                                                                                                                                                                                                                                                                       Sequence 2, Application US/08883036A
Patent No. 6672047
GENERAL INFORMATION:
APPLICANT: Rauch, Charles
APPLICANT: Walczak, Henning
TITLE OF INVENTION: Receptor That Binds TRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.2%;
Best Local Similarity 58.7%;
Matches 91; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)371-254
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION MABER: US/09/013,895A
FILING DATE: 27-JAN-1998
CURRENT APPLICATION DATA:
                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Superfamily and Binding to Trail (APO2-L) NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 PGACNRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCKPGTFRNDNSA 201
                MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Versic
                                                                                                                   COUNTRY: UZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 RVHKTFKFVV--VGVLLQVVPSSAATIKLHD---QSIGTQQWEHSPLGELCPPGSHRSER 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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CITY: ROCKVILLE
                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                          CITY: Seattle,
                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMCRKCSTGCPRGMVKVKDCTPWSDIECVHKESGN 236
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                                                                                                                                                                                           E: Kathryn A. Anderson,
51 University Street
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9410 KEY WEST AVENUE
                                                                                                                                     Sn
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              Version
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Pred. No. 7.5e-30;
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                  6.0.1
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PRIOR APPLICATION DATA:

CLASSIFICATION:

APPLICATION NUMBER: US/08/883,036A

26-JUN-1997

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US-09-333-593A-8
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                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DEEN, K
                                                                                                                                                                                                                                 Sequence 8, Application US/09333593A Patent No. 6313269
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Best Local
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APPLICANT: TRÜNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
                                                                                                                 APPLICANT: APPLICANT:
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TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      APPLICANT:
                                                                                                                                                                          APPLICANT:
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TYPODLOGY: lina
NOLECHT
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APPLICATION NUMBER: US 00
FILING DATE: 12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/799,861
FILING DATE: 13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                  212
                                                                                                                                                                                                                                                                                                                                                                                                                                           182 TMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYL 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 32.4%; Score 448; DB 3; Length 440; Local Similarity 40.7%; Pred. No. 5.5e-28; hes 105; Conservative 23; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 GRDCISCKYGQDYSTHWNDLLFCLRCTRCDSGEVELSPCTTTRNTVCQCEEGTFREEDSP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 RVPKTL--VLVVAAVLLIVSAESALITQQDLAPQQRAAPQQKRSSPSEGLCPPGHHISED 90
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REFERENCE/DOCKET NUMBER: 2625-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 28-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US --to be assigned--FILING DATE: 04-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGIIIGVTVAAVVLIVAV 229
                                                                                                                                                                                                                                                                                                                                                                                  SCTIVGIIVLIVLLIVFV 259
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                                                                                                                 ROSHAK, AMY K. TAN, KONG B.
                                                                                                                                                                      YOUNG, PETER R.
                                                                                                                                                      MARSHALL, LISA A.
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Query Match
Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 3.
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Best Local Similarity
Matches 89; Conserv
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                                                                                                                                                                                      SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/916,625
PRIOR ETILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/333,593A CURRENT FILING DATE: 1999-06-15 PRIOR APPLICATION NUMBER: 08/916,625
                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 424
TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                 LENGTH: 412
TYPE: PRT
                                                                                                                               ORGANISM: HOMO SAPIENS
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                                                                                                                                                                                                        FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09333593A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAN, KONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MARSHALL, LISA A. ROSHAK, AMY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEEN, KEITH C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                 Conservative
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               27.5%; Score 380.5; DB 4; 51.7%; Pred. No. 1.1e-22; rative 17; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.8%; Score 398.5; DB 4; 46.6%; Pred. No. 4.2e-24; ative 23; Mismatches 64;
                                                                                                                                                                                                                                                               60/041,230
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                                                   Length 412;
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; FEATURE:
NAME/KEY: XAA
; LOCATION: 410
; OTHER INFORMATION: XAA
US-09-329-633A-2
                                                                                                                                                                                                                                                                                                            US-09-079-029-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-329-633A-2
                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/089,253
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LEAVAGE: 1998-06-12
                                                                                                                                                                                                                                                                      Sequence 1, Application US/09079029 Patent No. 6342369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kim, K. Jin
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY
FILE REFERENCE: P1466R1 (REVISED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/329,633A CURRENT FILING DATE: 1999-06-10
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: human
                                                                                                                                                                       APPLICANT: Adams, Cami
APPLICANT: Ashkenazi,
APPLICANT: Chuntharapa
APPLICANT: Kim, Kyung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                        TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                151 EMCRKCRTGCPRGMVKVGDCTPWSDIECVHK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 EMCRKC-SRCPSGEVQVSNCTSWDDIQCVEE 152
                                                STREET: 1 DNA """
CITY: South San Francisco
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5. 6252050
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USA
94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78; Conservative
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                                                                                                                                                                                           Adams, Camilia W.
Ashkenazi, Avi J.
Chuntharapai, Anan
                                                                                                    Genentech, Inc.
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51.7%;
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; Pred. No. 1.3e-22;
17; Mismatches 53;
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           Query Match
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17.1%;

Score 236.5;

DB 4;

Length 303;

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RESULT 11
US-09-333-593A-4
; ORGANISM: HOMO SAPIENS US-09-333-593A-4
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                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Applic Patent No. 6313269
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Best Local
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
                                                                                       PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                    PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-(
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-(
                                                                                                                                                                                                                                                                                                 APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR.
TITLE OF INVENTION: TR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                   LENGTH: 30
TYPE: PRT
                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
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TYPE: Amino Acid
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                                                       303
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                                                                                                                                                                                                                                                                                                                                                                                                                  YOUNG, PETER R.
                                                                                                                                                                                                                                                                                                                                                             TAN, KONG
                                                                                                                                                                                                                                                                                                                                                                            MARSHALL, LISA A. ROSHAK, AMY K.
                                                                                                                                                                                                                                                                                                                                                                                                                                        DEEN, KEITH C
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51.7%;
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Pred. No. 1.
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ches 53;
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US-09-086-483A-4

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US-08-651-579-2
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                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 46; Conserva
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                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/651
FILING DATE: 22 MAY 1996
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VOUNG, JOHN A. T.
APPLICANT: YOUNG, JOHN A. T.
TITLE OF INVENTION: TUNOR VIRUS SUSCEPTIBILITY
TITLE OF INVENTION: PRODUCTS, AND USES RELATED
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-D
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
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120
                            127 KC-SRCPSGEVQVSNCTSWDDIQC 149
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                                                                           PCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSP-EMCR 126
                                                      PSKKD-EYTEYPNDFPKCLGCRTCREDQVEVSPCIPTRNTQCACKNGTFCLPDHPCEMCQ 119
                                                                                                                                                         LKFVVVIVAVLLPVLAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACN 67
                                                                                                                         LRLCPVLLLLFAEVQLGSAAAVKKRADRSDLQKPDLYR-----RKCPMGTYEANDSIQCL
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                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                 368 amino acids
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NAUGHTON, JOHN
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                               227-5941
                                                                                                                                                                                      15.3%; Score 212; DB 2;
31.9%; Pred. No. 1.9e-09;
tive 24; Mismatches 66
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9; Mismatches 18;
                                                                                                                                                                                          66;
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THERETO
                                                                                                                                                                                                                      Length 368;
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US-09-086-483A-4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/069,112
FILING DATE: Dec-9-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60
FILING DATE: May-30-97
FILING DATE: May-30-97
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LENGTH: 427 amino acids
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CORRESPONDENCE ADDRESS:
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249 DNLIPVYCSILAAVVVGLVAYI 270
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FILING DATE: May-29-98
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                                SPGTPASSHYLSCTIVGIIVLI 252
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                                                                                               SPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTT 230
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SYSTEM: PC-DOS/MS-DOS
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                                                                   --VVTTVMGSSQPVVTRG-TT
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RESULT 15
US-09-006-353A-5
Sequence 5, Application US/09006353A
Patent NO. 6261801
GENERAL INFORMATION:
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local S
Matches 64
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APPLICANT: Rabizadeh,
TITLE OF INVENTION: PO
TITLE OF INVENTION: PO
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CORRESPONDENCE ADDRESS:
APPLICANT:
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SYSTEM: PC-DOS/MS-DOS
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Search completed: August 13, Job time: 65 sec
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Best Local
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CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROCKES, ANDERS A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353
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ADDRESSEE: HUMAN GENOME SCIENCES,
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
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TOPOLOGY: li
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GENTZ, REINER
RUBEN, STEVEN
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24.48;
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                 2002, 08:30:31
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 201.5; DB 4;
Pred. No. 1.5e-08;
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A Geneseq_032802:*

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9: /SIDSI/gcgdat/
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10: /SIDSI/gcgd/
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No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747574 seqs, 111073796 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSPGTPAPAAEETMTTSPG 19
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
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AAW64668
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AAB201111
AAB36696
AAB53691
AAB53691
AAB53691
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                                                                                                                  Human
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                                                                                                                                                                                                      Human hAPO9
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                                                                                                            n hAPO9 protei
n Apo-2DcR pro
n PRO366 polyp
n immunostimul
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.0 191 22	47.0 191	48.0 1469 22	8 48.0 1466 22	48.0 1196 13	8 48.0 1078 21	48.0 1078 16	8 48.0 259 22	.0 238	48.0 189 22	48.0 152 22	48.5 602 21	48.5 258 22	48.5 258 22	48.5 258 21	49.0 907 22	9 49.0 761 22	49.0 167 22	51.0 2066 22	51.0 219 22	52.0 221 22	53.0 536 21	801 22	54.0 440 21	54.0 440 20	54.0 440 19	54.0 440 19	54.0 350 20	100.0 299	100.0 299 20	100.0 299 20	100.0 299	100.0 299 20 AAY	
Drosophila melanog	Drosophila melanog	=				alp	human	Novel human diagno	Novel human diagno	Propionibacterium	Human 2ntr2 protei	Protein of the inv	Human PRO polypept	PRO130	human	human	Novel human secret	Streptomyces nours	Propionibacterium	Propionibacterium	Macaca mulatta rha		TNF-related apopot	necrosis	ĸ	~			Human Apo-2DcR pro	TNF-relat	Human TRAIL-R3 pro	to.	Human secreted pro

## ALIGNMENTS

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RESULT
AAB82182
FLAG-epitope tag; transmembrane domain; death domain; apoptosis; cell suicide; tissue homeostasis; cell proliferation; cell-cell signalling; Trail Receptor without Intracellular Domain; TRID
                         23-AUG-2000; 2000WO-US23112.
                                                                                          Misc-difference
                                                                                                                                                             Key
                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                   FLAG-TRID clone without a transmembrane domain
                                                                                                                                                                                                                                                       23-JUL-2001
                                                                                                                                                                                                                                                                          AAB82182;
                                                                                                                                                                                                                                                                                         AAB82182 standard; Protein;
        25-AUG-1999;
                                             01-MAR-2001
                                                                WO200114542-A1.
                                                                                                             Peptide
                                                                                                                                Protein
                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                              Н
                                                                                                                                                                                                                                                       (first entry)
        99US-0150747
                                                                                         /label= FLAG-epitope
249
                                                                                                             /label= Signal_peptide
24..249
/label= FLAG-TRID
27..34
                                                                                  /note= "Insertion site for candidate sequences"
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                             249
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Human tumour necro Human angiogenesis FLAG-TRID clone wi

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RESULT
AAW64668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC domain (TM) of a membrane spanning protein. The method comprises
CC modifying a nucleic acid encoding a death domain (DD) lacking membrane
CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID)
CC by replacing the nucleic acid encoding the TM of the DD-lacking
CC membrane spanning protein with a candidate nucleic acid sequence to
CC produce a nucleic acid encoding a modified DD-lacking membrane spanning
CC protein. The modified nucleic acid is then transfected into a host cell,
CC which expresses a DD-containing receptor. The absence of apoptosis of the
CC host cell is determined following exposure of the transfected cell to an
CC apoptosis inducing ligand. Candidate nucleic acids encoding TM prevent
CC modified death domain-lacking membrane-spanning protein can also include
CC modified death domain-lacking membrane-spanning protein can also include
CC a FLAG-TRID clone, which was used in the method of the present sequence is
CC a FLAG-TRID clone, which was used in the method of the present invention.
CC This sequence comprises human TRID protein and the FLAG-epitope tag. The
CC FLAG-epitope is a useful marker to purify proteins encoded by the
CC modified DD-lacking membrane-spanning protein. The identified TM and
CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat
CC events, such as cell proliferation and cell-cell signalling pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                             Homo
                                                                                                                                                                                   TRAIL receptor without intracellular domain; TRID; TNFR-5; human; tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a transmembrane domain of a membrane-spanning protein useful in defining processes in cell suicide and tissue homeostasis, comprises modifying the nucleic acid encoding a death domain-lacking
                Region
                                            Region
                                                                      Protein
                                                                                                  Peptide
                                                                                                                 Кeу
                                                                                                                                                                       haematopoietic
                                                                                                                                                                                                                              Human TRID protein.
                                                                                                                                                                                                                                                           23-OCT-1998
                                                                                                                                                                                                                                                                                       AAW64668;
                                                                                                                                                                                                                                                                                                                AAW64668 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                      s factor
tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,
/label= epitope
58..66
/label= epitope
                                          /label= TRID
42..52
                                                                     /label- signal
27..259
                                                                                                              Location/Qualifiers
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                                                                                                                                                                       system;
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0;
                                                                                                                                                                       apoptosis; treatment
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                therapy
                                                                                   19-JUL-1999
                                                                                                               AAY05726;
                                                                                                                                          AAY05726
                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ebner
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14-JAN-1997;
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disorders, substantially altered (whether increased or decreased) levels of TRID gene expression can be detected, therefore the TRID polypeptides, nucleic acids and antibodies are useful in the diagnosis of such immune system related disorders. Mutations of the TRID gene can also be detected. TRID can also be used to identify ligands which may be useful in the treatment of apoptosis related disorders. TRID is administered to humans at a parenteral dose of 0.01 to 1 mg/kg/day.
                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a human TRID (TRAIL (TNF-related apoptosis-inducing ligand) receptor without an intracellular domain). TRID is a member of the tumour necrosis factor receptor (TNFR) family also known as TNFR-5. TRID is expressed in haematopoletic tissues and other normal human tissues. For a number of immune system related other normal human tissues.
TRAIL-3; tumour necrosis factor receptor; apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TRAIL receptor without an intracellular domain polypeptide used in the diagnosis of immune system·related disorder(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV51348
                           Tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-399141/34
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                                                                                                                                                                          tspgtpapaaeetmttspg
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                                                                                                                                                                                                                              l Similarity 100
19; Conservative
                                                                                                          standard;
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                                                    (first entry)
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97US-0035496
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/label=
79..85
/label=
91..102
                          factor receptor TRAIL-R3
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142..148
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                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gentz RL,
                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                            Score 100; DB 12,
Pred. No. 5.4e-05;
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                                                                                                                                                                                                                                                    Length
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Mammalia

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                                                                                                                                                                                                                               The present sequence represents TRAIL-R3, a novel mammalian cysteine-rich receptor of the tumour necrosis factor receptor family. Crysteine-rich receptor of the tumour necrosis factor receptor TRAIL, i.e. TRAIL-2 The invention is related to novel receptors for TRAIL, i.e. TRAIL-2 Cree AAY05725) and TRAIL-3. TRAIL-3 is highly glycosylated. It is a putative glycosylphosphatidylinositol-anchored protein, which is ceither cell-associated or processed and secreted. Secreted TRAIL-R3 competes for the binding of TRAIL to TRAIL-R1 and/or TRAIL-R2, thereby acting as an inhibitor of apoptosis. Expression of TRAIL-R2, thereby acting as an inhibitor of apoptosis. Expression of TRAIL-R3 is restricted to peripheral blood lymphocytes and composite the second of the analysis of the advancement, severity or effects of an immunological disease involves administering a TRAIL-R2 or TRAIL-R3 blocking agent such as a soluble TRAIL-R (preferably a method of treating cancer involves administration of antibodies against TRAIL-R3 or TRAIL-R2. A method of intodies capable the second of the 
                                                                                       Query Match
Best Local
                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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N-PSDB; AAX25349.
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12-SEP-1997;
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 185
                                   1 TSPGTPAPAAEETMTTSPG
 tspgtpapaaeetmttspg
                                                                       Similarity
19; Conser
                                                                                                                                                                                                  s administration of of TRAIL-R2 or -R3
                                                                                                                                                                259
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                                                                       Conservative
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162..175
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Pred. No. 5.4e-05;
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185

1 TSPGTPAPAAEETMTTSPG tspgtpapaaeetmttspg

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AAW93578
                                                                                                                                               CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TWF related ligands 1 and 3 (TNRL1 and TNRL3) or CC their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 is useful for identifying selective by determining levels of APO4 is useful for identifying selective be treated using APO4 selective binding agents linked to a therapeutic CC molety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of CC agents to the polypeptide/active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC or agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or CC treatment of disease are also identified using APO4 polypeptides/active CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vitro. APO6 polypeptides are also indendified using APO4 polypeptides are also indendified using APO4 is also CC are all useful as immunogens for preparing antibodies. APO4 is also constraints. APO8 was transfected to human breast carcinoma cell line CC abnormalities. APO8 was transfected to human breast carcinoma cell line
   Matches
                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
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                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 24; Fig 6; 156pp; English.
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N-PSDB; AAX23412.
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Score 100; DB 20;
Pred. No. 5.4e-05;
Mismatches 0;
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AAW88408

XX AAW88408

XX AAW8

YFT Pep

FTT ASH

XX New

PTT ABN

XX New

PTT ABN

CCC Itut

CCC off
This polypeptide comprises human Apo-2DcR, a novel member of the tumour necrosis factor receptor family that binds to Apo-2 ligand. The samino acid sequence was deduced from the nucleotide sequence of an isolated cDNA clone (see AAV84347); an alternative translation
                                                                         New Apo-2DcR polypeptide - used for apoptosis, e.g. in neurodegeneration
                                                                                                                     WPI; 1999-095340/08
                                                     Claim 1; Page 50-51;
                                                                                                                                                   Ashkenazi AJ,
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192..206
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n; autoimmune disease; inflammation; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           initiation site in this clone will encode a polypeptide (see AANA88409) comprising amino acid residues -40 to 269 of Apo-2DcR shows more sequence identity to DR4 (60%) and Apo-2 (50%) than to other apoptosis-linked receptors. The polypeptide can be obtained by expression in host cells using the vector deposited as ATCC 209087. The invention provides vectors and host cells for recombinant production of Apo-2DcR polypeptides, antibodies, and transgenic and knockout animals (useful e.g. for screening and developing drugs that protect against excessive apoptosis). Apo-2DcR, or chimeras comprising Apo-2DcR or its (claimed) cextracellular domain fused to a heterologous polypeptide are used to modulate apoptosis of mammalian cells (claimed) and/or NF-kappaB activation by Apo-2 ligand, and may be expressed in vivo or ex vivo for gene therapy. They can be used in methods for the modulation and diagnosis of apoptosis e.g. in cases of neurodegeneration, cand diagnosis of apoptosis e.g. in cases of neurodegeneration, cand candense diseases and inflammation. Most human tumour cells do not express Apo-2DcR transcripts, but normal tissues do, suggesting that Apo-2DcR may permit selective killing of cancer cells by Apo-2 ligand, possibly by protecting normal, but not cancerous, cells.
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Best Local S
Matches 19
16-DEC-1999
20-DEC-1999
20-DEC-1999
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06-JAN-2000
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09-DEC-1999
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2000WO-US01277.
2000WO-US03265.
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2000WO-US03414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMU12172-AAU12446 represent novel human secretory and transmembrane CC PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by Skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide CC molecules involved in binding interactions. The polynucleotides encoding CC PRO polypeptides can be used to generate probes, antisense RNA/DNA, cc transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000;
02-JUN-2000;
10-NOV-2000;
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20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
22-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
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                        PRO366; UNQ321; human; immune disease; autoimmune antirheumatic; antiarthritic; antiinflammatory; ar immunosuppressive; antithyroid; antidiabetic; neur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO
                                                                                                                                                                                                                                                                                             AAB20111 standard; Protein; 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH
                                                                                                                                                                                     30-APR-2001
                                                                                                                                                                                                                                         AAB20111;
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                                                                                                                                                                                                                                                                                                                                                                                                                              185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TSPGTPAPAAEETMTTSPG
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                                                                                                                                                                                                                                                                                                                                                 7
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DB; AAS21393.
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Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beresini M,
Æ, Goddard
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2000WO-US07337.

2000WO-US07532.

2000WO-US08439.

2000WO-US13705.

2000WO-US14042.

2000WO-US14941.

2000WO-US15564.

2000WO-US15564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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                                                                                                                              PRO366 (Apo-2DcR).
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Tumas
dermatological; antipsoriatic;
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A, Godowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 100; DB 22;
Pred. No. 5.4e-05;
; Mismatches 0;
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ski PJ, Gurney i
Watanabe CK, W
                           neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood WI,
                                                 antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Filvaroff E,
L, Sherwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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Apo-2006 shows homelogy to apoptosis-linked receptors of the tumour checking factor receptor family, such as DR4 and Apo-2. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAF30108-20) including PRO366. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, comprising a property cells into a tissue of a mammal, comprising a property cells into a tissue of a mammal, comprising a property cells into a tissue of a mammal, comprising a property compositions comprising a property of the apoptosite of T-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising a PRO polypeptide or its antagonist comprising a PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, the disorder is selected from systemic lupus erythematosus, composition in the property of the disorder is systemic sclerosis, idiopathic inflammatory compositions of the property of the disorder is systemic sclerosis, idiopathic inflammatory compositions of the property of the property of the disorder is syndrome, systemic vasculitis, sarcoidosis, autoimmune thrombocytopaenia, autoimmune autoimmun
                                                                                                                                                                                                                                                                                                                                                                        The present sequence is Apo-2DcR, a novel human deduced from a human bre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PRO polypeptides, nucleic acids and (ant)agonists, diagnosing and treating immune-related disorders, such sclerosis, rheumatoid arthritis and diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ,
                                                                                                                                                                                                                                                                                                                                                                        sequence is that of PRO366 (UNQ321), also designated novel human immunomodulator (27 kDa, pI 4.84), as a human breast carcinoma cDNA clone (see AAF30053).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mark MR,
diabetes mellitus,
diseases (such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0144758
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114..1
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72..78
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126..1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      127pp;
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Marsters
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phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
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  multiple
                    immune-mediated renal
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Pitti RM,
  sclerosis),
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Tumas D, Watanabe
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ID AAB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antiinflammatory; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder;
The present sequence represents the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor
                                                                                                                Claim
                                                                                                                                                                                                                                                                                  N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-2000
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                                                                                                                                                                       prevention
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                                                                                                                                                                                                                        acid encoding
                                                                                                                                                                                                                                                                                                                                                                   Ruben
                                                                                                                                                                                                                                                                                  AAC90774.
                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN GENOME SCI
                                                                                                                                                            acid encoding a TRID polypeptide, also referred to as tumor factor receptor 5, useful in the diagnosis, treatment or on of cancer, autoimmune disorders and viral infection -
                                                                                                          Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259
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                                                                                                                                                                                                                                                                                                                                                                SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0135164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder; viral infection
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                                                                                                        285pp; English
                                                                                                                                                                                                                                                                                                                                                                   Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor 5 (TRID) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 22;
Pred. No. 5.4e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259;
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Best Local
                                                                                                                                                                         15-SEP-1999;
05-OCT-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1999;
14-MAY-1999;
02-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; angiogenesis-associated protein; PRO; endothelial cell growt cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins an polynucleotides are useful in the treatment of tumours, resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crohn's disease; psoriasis; endometriosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parasite, bacteria and viruses, restenosis and graft versus host diseas
They are also useful for inducing proliferation of T-cells, endothelial
                                                                                                                               30-NOV-1999
                                                                                                                                                                                                                                                                                                             15-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                      08-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                                                                         01-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease; Huntington's disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human angiogenesis-associated protein PRO366, SEQ ID NO:152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
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19; Conserv
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                                                                                                                                                                                                                      99WO-US21090.
99WO-US21547.
99WO-US23089.
                                                                                                                                                                                                                                                                                                                                                                                           99WO-US12252.
99US-0141037.
99US-0144758.
99US-0145698.
99WO-US20111.
                                                                                                                               99WO-US28313
99WO-US28409
                                                                                                                                                                                                                                                                                                                                                  99WO-US20594.
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990S-0134287
                                                                                           99WO-US28564
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Pred. No. 5.4e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRID proteins and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the CC administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO CC agonists and PRO antagonists may be used as therapeutic agents to treat CC ardiovascular, endothelial or angiogenic disorders, such as CC atherosclerosis, osteoporosis, myocardial infarction, hypertension, CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, PRO ricelia, CC disease, or stroke. PRO nucleic acids are additionally useful in the CC screen libraries to isolate cDNAs with sequence identity to PRO proteins, CC to map genes encoding PRO proteins, to analyse genetic disorders, and in CC gene therapy. PRO nucleic acids can also be used to produce transgenic annuals useful for the development and screening of potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer -
                          FLAG-epitope tag; transmembrane domain; death domain; apoptosis; cell suicide; tissue homeostasis; cell proliferation; cell-cell signalling; Trail Receptor without Intracellular Domain; TRID.
                                                                                                                                                           FLAG-TRID clone with a transmembrane
                                                                                                                                                                                                                          23-JUL-2001
                                                                                                                                                                                                                                                                                         AAB82181;
                                                                                                                                                                                                                                                                                                                                                     AAB82181 standard; Protein; 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TSPGTPAPAAEETMTTSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-090793/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tspgtpapaaeetmttspg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69; Fig 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Gurney AL,
Pitti RM, Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agents.
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara N,
Hillan KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100; DB 22;
Pred. No. 5.4e-05;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Gerber H, Goddaı
, Kuo SS, Mark MR,
Williams PM, Wood
                                                                                                                                                           domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goddard A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a PRO pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marsters SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding
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RESULT
AAW76331
ID AAW
XX
AC AAW

AAW76331 standard;

Protein;

299

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11

AAW76331;

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Gaps

0,

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cc spanning protein (e.g. Trail Receptor without intracellular Domain; TRID)

Cc by replacing the nucleic acid encoding the TM of the DD-lacking

cc membrane-spanning protein with a candidate nucleic acid sequence to

cc produce a nucleic acid encoding a modified DD-lacking membrane spanning

cc protein. The modified nucleic acid is then transfected into a host cell,

cc which expresses a DD-containing receptor. The absence of apoptosis of the

cc host cell is determined following exposure of the transfected cell to an

cc apoptosis oinducing ligand. Candidate nucleic acids encoding TM prevent

cc apoptosis of the host cell. The modified nucleic acid encoding the

cc modified death domain-lacking membrane-spanning protein can also include

a nucleic acid sequence encoding an epitope tag. The present sequence is

ca FLAG-TRID clone, which was used in the method of the present invention.

Cc FLAG-epitope is a useful marker to purify proteins encoded by the

cc modified DD-lacking membrane-spanning protein. The identified TM and

cc membrane-spanning proteins may be used in defining processes involved in

cc ell suicide and tissue homeostasis, and to evaluate, interfere and treat
                                                                                                                 Matches
                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a transmembrane domain of a membrane-spanning protein useful in defining processes in cell suicide and tissue homeostasis, comprises modifying the nucleic acid encoding a death domain-lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain (TM) of a membrane-spanning protein. The method comprises modifying a nucleic acid encoding a death domain (DD) lacking membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane spanning protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAH19325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001
                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to methods for identifying a transmembrane domain (TM) of a membrane-spanning protein. The method comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Denome SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                            events, such as cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
194
                                                                                                                                             Local Similarity
                           1 TSPGTPAPAAEETMTTSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-374162/39
                                                                                                                 19;
                                                                                                                                                                                                                                                                  268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swain PM,
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US23112
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27..34
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24..268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= FLAG-eptitope_TAG
250..268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                      proliferation and cell-cell signalling pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tzellas N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal_peptide
                                                       19
                                                                                                              0;
                                                                                                           Score 100; DB 22;
Pred. No. 5.5e-05;
Mismatches 0;
                                                                                                                 Indels
                                                                                                                                                                     Length
                                                                                                                                                                            268;
                                                                                                                 0,
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11-JAN-1999

(first entry)

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CC protein that has a membrane proximal O-glycosylation region. The CC invention provides methods for the recombinant production of TR5 CC and its use in diagnostic and therapeutic methods. Treatment of a CC subject in need of enhanced TR5 activity comprises administering an CC form so as to effect production of the polypeptide in a CC form so as to effect production of the polypeptide activity in vivo. CC Treatment of a subject with the need to inhibit TR5 polypeptide activity comprises administering an antagonist to the polypeptide activity comprises administering a polypeptide for its ligand, substrate or receptor. Diagnosing a disease or a susceptibility comprises determining the presence or absence of mutation in the comprises determining the presence or absence of mutation in the genome of the subject and/or analysing for the presence or amount of TR5 compounds compound and assessing the ability of it to bind to the cells. The cartive agents can be used for the treatment of chronic and acute confidence of inflammation, arthritis, septicaemia, autoimmune diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent and treat e.g. inflammation, arthritis, septicaemia, autolumune diseases, infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury, AIDS and bone diseases
graft vs host disease, infection, stroke, ischae respiratory disease syndrome, restenosis, brain diseases, cancer (e.g. lymphoproliferative disordiseases, cancer (e.g. lymphoproliferative disordiseases)
                                                                                                         inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1997;
05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP867509-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stroke; ischaemia; acute respiratory disease syndrome; psoriasis;
restenosis; brain injury; AIDS; bone disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is the amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1998-497862/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see AAV56990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     necrosis related receptor; TR5; human;
tis; septicaemia; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TR5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epticaemia; transplant rejection; autoimmune disease; bowel disease; graft versus host disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           necrosis related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0795910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98EP-0300827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Truneh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BEECHAM CORP
              lymphoproliferative disorders),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ed from the sequence of an isolated cDNA
The protein is characterised as a GPI-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor
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                                                                                ischaemia,
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RESULT 1
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Best Local
as nutritional sources or supplements. Such uses include use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. They may also have utility in compositions used for bone, cartilage, tendon, ligament, and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and
                                                                                                                                                                 although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity haematopoiesis regulating activity, tissue growth activity, haemostati activiny/inhibin activity, chemotactic/chemokinetic activity, haemostati and thrombolytic activity, receptor/ligand activity, and tumour activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides and proteins can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs K,
Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-1998;
14-MAY-1998;
10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                              sequences. AAZ21103 to AAZ21112 represent probes for the secreted proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ21093 to AAZ21102 encode new human secreted proteins and AAY29861 to AAY29873 represent the secreted proteins encoded by the polynucleotide sequences. AAZ21103 to AAZ21112 represent probes for the secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 104; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotides encoding secreted human proteins, de fetal brain, human adult blood, human adult bladder, neural tissue cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ21096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-551362/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted
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99US-0266105
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າ MJ,
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Pred. No. 6.1e-05;
; Mismatches 0;
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Steininger RJ;
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The present sequence represents tumour necrosis factor receptor (TNFR) TR5, also known as TRID or DCR1. The invention relates to TNFR related polypeptides TR1, TR3 and TR5 (see AAX05742-44) and their ligand TL3 (see AAX05745). TR1, TR3, TR5 and TL3 are used in claimed methods of identifying agonists and antagonists, i.e. compounds that bind to the receptors or ligand, and which activate (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for identifying agonists, antagonists, ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The agonists and antagonists are useful for treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune disease e.g. inflammatory bowel disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis and Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor receptor; TR5; TRID; DcR1; agonist; antagonist; screening; human; cancer; AIDS; Alzheimer's dise; inflammation; arthritis; septicaemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; restenosis; brain injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ulcers. The proteins which induce cartilage and/or bone growth in circumstances where bone is not normally formed, have application in the healing of bone fractures and cartilage damage or defects in humans and other animals.
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                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                               Identifying agonists and antagonists of tumor necrosis factor related receptors {\tt TR1}, {\tt TR3} and {\tt TR5}, and of ligand {\tt TL3}, useful
                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                               McDonnell
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19; Conser
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                                                                                                                                                                                                                                                                     Page 13-14; 23pp;
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                                                                                                                                                                                                                                                                                                      cancer,
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                                                                                                                                                                                                                                                                                                    Alzheimer's disease,
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Pred. No. 6.1e-05;
Mismatches 0;
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                                       This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An CC antibody against the TRAIL receptors is useful for detecting mammalian CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins. CC (Ant)agonists identified by the assay are useful for modulating the cappototic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis crelated conditions which are treated in this way, include cancer CC (e.g. Lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus crythematosus and immune-mediated glomerulonephritis), viral infections CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders CC (e.g. hkzheimer's disease and Parkinson's disease), amyotrophic lateral CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial confarction and stroke). The polynucleotides can also be used to treat these diseases. Antisense oligonucleotides to the DNA sequences can be used to form a composition that is useful for inhibiting expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
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                                                                                                                                                                                                                                                                                                                                            Newly isolated polynucleotide encoding a mammalian TRAIL receptor protein - useful in for screening for (ant)agonists that modulate the apoptotic activity mediated by DR5 or TRAIL-R3 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; DR5; DR5s; TRAIL-R3; apoptosis related condition; ca
autoimmune disease; viral infection; degenerative disorder;
amyotrophic lateral sclerosis; retinitis pigmentosa; ischae
cerebellar degeneration; myelodysplastic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease,
                                                                                                                                                                                                                                                                                                               Claim 16; Page 62-63; 71pp; English.
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DB; AAX27280.
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19; Conservative
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                             or TRAIL-R3
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is human tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be used for inhibiting the biological activities of TRAIL or for purifying TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated disorder such as T cell death in HIV-infected patients. They can be used for treating thrombotic microangiopathies such as thrombotic thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic acids can also be used for gene therapy. They can also be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated TRAIL binding protein - which binds to a tumour necrosis factor-related apoptosis inducing ligand, used in the diagnosis and treatment of TRAIL-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; TNF-related apoptosis-inducing ligand binding protein; clotting; TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy; thrombotic microangiopathy; thrombotic thrombocytopenic purpura;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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RESULT 2 T21621 T21621 T21621 T21621 C;Species: Caenorhabdit1s elegans C;Species: Caenorhabdit1s elegans C;Species: Caenorhabdit1s elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T21621 R;Kershaw, J. Submitted to the EMBL Data Library, November 1996 A;Reference number: Z19451 A;Reference number: Z19451 A;Accession: T21621 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-878 <wil>A;Cross-references: EMBL:Z83107; PIDN:CAB05498.1; GSPDB:GN00019 A;Cross-references: EMBL:Z83107; PIDN:CAB05498.1; GSPDB:GN00019 C;Genetics: A;Gene: CESP:F32A7.5 A;Introns: 74/3; 380/3; 439/3; 567/3; 728/3; 818/1</wil>	Query Match Best Local Similarity 76.9%; Pred. No. 26; Matches 10; Conservative 1; Mismatches 2; Ind.  Qy 6 PAPAAEETMTTSP 18	RESULT 1 T29018 hypothetical protein ZK84.1 - Caenorhabditis elegans C; Species; Caenorhabditis elegans C; Species; Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C; Accession: T29018 R;Kirsten, J. submitted to the EMBL Data Library, April 1995 A; Description: The sequence of C. elegans cosmid ZK84. A; Reference number: Z20553 A; Accession: T29018 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-801 <kir> A; Cross-references: EMBL:023181; PIDN:AAC48204.1; GSPDB:GN00020; A; Experimental source: strain Bristol N2; clone ZK84 C; Genetics: A; Genetics: A; Map position: 2 A; Introns: 22/2; 45/3; 108/1 A; Map position: 2 A; Superfamily: collagen alpha 1(I) chain; fibrillar collagen car</kir>	ALIGNMENTS	30 46 46.0 2440 2 S39162 31 46 46.0 7463 2 T36248 32 45.5 45.5 223 1 MFVNSV 33 45.5 45.5 583 2 F69153 34 45.5 45.5 583 2 T18664 35 45.5 45.5 2105 2 T18668 36 45 45.0 340 2 C70743 37 45 45.0 340 2 C70743 38 45 45.0 429 2 A48377 39 45 45.0 429 2 A48377 40 45 45.0 459 2 A56954 41 45 45.0 548 2 T27542 42 45 45.0 548 2 T27542 43 45 45.0 632 2 S42731 44 45 45.0 736 2 T25447 44 45 45.0 736 2 T25663 45 45.0 1176 2 A49848
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C;Species: Rattus norvegicus (Norway rat)
C;Becies: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S24169
R;Huan, L.J.; Xu, G.; Forstner, G.; Forstner, J.
Biochim. Biophys. Acta 1132, 79-82, 1992
A;Title: A serine, threenine and proline-rich region near the carboxyl-term. A;Reference number: S24169; MUID:92379096
A;Accession: S24169; MUID:92379096
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T3
   A;Note: host Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 16-Jun-2000
C;Accession: A00781; C30083
                                                                                            N;Alternate names: gene UL12 protein C;Species: human herpesvirus 1
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A; Residues: 1-292 <HUI
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C; Keywords:
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A;Title: The murine Ki-67 cell proliferation antigen
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A; Residues: 1-2938 <STA>
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R;Starborg, M.; Gell, K.; Brundell, E.;
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2; Mismatches
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                                                            RESULT
S20963
homeotic protein Hox B3 - mo N; Alternate names: homeotic
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A;Gene: TP0863
C;Superfamily: nitrogen fixation protein nifS
C;Keywords: phosphoprotein; pyridoxal phosphate; sulfurtransferase
F;232/Binding site: pyridoxal phosphate (Lys) (covalent) #status pr
F;374/Active site: Cys (cysteine persulfide intermediate) #status pr
                                                                                                                                                                                                                                                                                                                                                                                        they, L.; Weidman, J.; Smith Science 281, 375-388, 1998 A;Title: Complete genome sec A; Reference number: A/1250; A; Accession: G71272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iron-sulfur cofactor synthesis protein nifs2 TP0863 [similarity] - syphilis spirochet N;Contains: L-Cysteine sulfurtransferase (EC 2.8.1.-) C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 20-Jun-2000 C;Accession: G71272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:X03839; NID:g59841; PIDN R;MCGeoch, D.J.; Dalrymple, M.A.; Davison, A.J. J. Gen. Virol. 69, 1531-1574, 1988 A;Title: The complete DNA sequence of the long A;Reference number: A30083; MUID:88274327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;McGeoch, D.J.; Dolan, A.; Frame, M.C. Nucleic Acids Res. 14, 3435-3448, 1996 A;Title: DNA sequence of the region in the A;Reference number: A93620; MUID:86205244 A;Accession: A00781
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                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE001256; GB:AE000520; A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uti they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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C;Superfamily: herpesvirus exonuclease
C;Keywords: exonuclease; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-626 <MC2>
A; Cross-references: GB:X14112;
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A; Residues: 1-626 < MCG>
                                                                                                                                                                                                                                                                              C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; nucleic
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TPPGYPAPTAQRALTYS
                                      TSPGTPAPAAEETMTTS
                                                                             Similarity
9; Conserv
                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               sequence of Treponema
30; MUID:98332770
                                                                                                48.0%;
52.9%;
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    225
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                                                                                                Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                        sequence
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47;
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                                                                                                                  Length 427
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mouse c protein

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C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 20-Aug-1999
C;Accession: S20963; D42694
R;Sham, M.H.; Hunt, P.; Nonchev, S.; Papalopulu, N.; Graham, A.; Boncinelli
EMBO J. 11, 1825-1836, 1992
A;Title: Analysis of the murine Hox-2.7 gene: conserved alternative transcr
A;Reference number: S20963; MUID:92258392
A;Accession: S20963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F39H11.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T22002 R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: sequence extracted from NCBI backbone (NCBIN:92310, NCBIP:92316) C;Superfamily: homeotic protein Hox B3; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;192-248/Domain: homeobox homology <HOX>
                                   C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Accession: T21700
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                                                                                 RESULT 9
T21700
hypothetical protein F33E2.6 - Caenorhabditis elegans
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A; Residues: 1-433 <SH
   R; Lennard, submitted
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A; Introns: 109/3; 154/1;
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Pred. No. 73;
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January 1997
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A; Residues: 1-846 <WIL>
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                                                                                                                                   A; Status: preliminary
                                                                                                                                                    A; Reference number: A; Accession: S05272
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A; Residues: 1-1323
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A; Reference
                                   A; Title: Structure
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S04642; MUID:89350838
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R;Prockop, D.J.
submitted to the EMBL Data Library, February 1989
A:Reference number: S05272
                                                                                                                                                                                                                                                           collagen alpha 1(III) chain precursor - human
N;Alternate names: procollagen alpha 1(III) chain
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spalt protein - mouse (fragment)
N;Alternate names: zinc finger protein msal
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
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                  A; Molecule type: mRNA
A; Residues: 1-1240, 'V', 1242-1466 <PRC>
A; Cross-references: EMBL: X14420; NID:g3005
R; Ala-Kokko, L.; Kontusaari, S.; Baldwin,
Biochem. J. 260, 509-516, 1989
                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868; S59511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: The mouse homolog of the region specific homeotic A; Reference number: 220791; MUID:96391179
A; Accession: T30253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: X97581; NID: g1296844; PIDN: CAA66196.1;
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50.0%;
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                                     NID:g30057; PIDN:CAA32583.1; PI
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A;Cross-references: GB:S62925; NID:g386425; IR;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; EBiochem. J. 311, 939-943, 1995
A;Title: Abnormal type III collagen produced A;Reference number: S59511; MUID:96067614
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A;Title: Cloning and analysis of the 5' portion A;Reference number: PE0011; MUID:89378752
A;Accession: PE0011
                                                                   A; Molecule type: mRNA
A; Residues: 302-423 <CHI>
A; Cross-references: GB:S79877; NID:g11955
A; Csyer, J.M.; Kang, A.H.
Blochemistry 17, 3404-3411, 1978
A; Title: Covalent structure of collagen:
A; Reference number: A90414; MUID:79000343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 149-163,'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,
A; Cross-references: EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:g930045
A; Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide
R; Seyer, J.M.; Kang, A.H.
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Nucleic Acids Res. 17, 6742, 1989
A;Title: Nucleotide and amino acid sequences
A;Reference number: S04887; MUID:89386015
A;Accession: S04887.
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A; Note: author submitted corrections to A90399
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A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398
A;Experimental source: liver
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A; Title: Covalent structure of collagen: amino
A; Reference number: A90399; MUID: 77134724
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A;Title: Nucleotide sequence of a cDNA coding A;Reference number: S01726; MUID:88303360
A; Molecule type: protein A; Residues: 399-675, 'N',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398
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A; Accession: A94562
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A; Residues: 1-176 <BEN>
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A;Note: the complete sequence is not shown
R;Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
                                                   A; Accession: A90414
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A; Residues: 1-170 <TOM>
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'N',677-727
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R:Lee, B.; Vitale, E.; Superti-Furga, A.; St
J. Biol. Chem. 266, 5256-5259, 1991
A;Title: G to T transversion at position +5
A;Reference number: 155349; MUID:91161621
A;Accession: 155349
A;Cross-references: GB:M11134;
R;Chu, M.L.; Weil, D.; de Wet,
J. Biol. Chem. 260, 4357-4363,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1065-1155,'p',1157-1466 <LOI>
A; Cross-references: EMBL:X01655; EMBL:X01742; N
R; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman,
Biochemistry 25, 1408-1413, 1986
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R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.;
R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.;
Ruccleic Acids Res. 12, 9383-9394, 1984
A;Title: Molecular cloning and carboxyl-propeptide analysis of human
A;Reference number: A93551; MUID:85087944
A;Accession: A93551
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A;Accession: A90446
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A;Molecule type: DNA
A;Residues: 537-605 cLEE>
A;Cross:references: GB.M59312; NID:g180815;
R;Seyer, J.M.; Mainardi, C.; Kang, A.H.
                                                                                                                                                                               A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C. Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985 A;Title: Human alpha I(III) and alpha 2(V) procollagen genes A;Reference number: 159025; MUID:85216505
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A; Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466
A; Cross-references: EMBL: X06700; NID: 930053; PIDN
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A;Title: Human pro alphal(III) collagen: cDNA sequence for the 3'A;Reference number: S02119; MUID:88189827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: liver
R;Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; C
J. Biol. Chem. 265, 17070-17077, 1990
A;Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping
A;Reference number: A38303; MUID:91009133
A;Accession: A38303
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A; Accession: A90438
                                                                               A; Molecule type: mRNA
A; Residues: 1165-1196 <EMA>
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A; Residues: 1161-1200 <MIS>
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A; Residues: 965-979,'A',981-984,'PS',987,'QN',990-1096,'P',1098-1152,'AT',1155,'S',11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
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A; Residues: 861-1015
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A; Residues: 728-895, 'A', 897-964 <SEY4>
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Biochemistry 19, 1583-1589, 1980
                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
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1985
                      NID:g180417;
W.; Bernard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino
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                      M.; Sippola, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g29584; PIDN:CAA25821 n, B.; Rennard, S.I.; Tols:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid sequence of alpha1 (III)-CB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid
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                                                                                                                                                                                                                                                                                               PID:g180416
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                         PID:g180418
Ramirez, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:g180816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:AAB59383.1; PI with Ehlers-Danlos
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Isolation

0f

cDNA and

genomic

clones encoding

human

pro-alphal(III)

collagen

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Fil197-1221/Region: carboxyl-terminal nonhelical telopeptide
F;1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted
F;151/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;161,1212/Modified site: allysine (Lys) #status predicted
F;161,1212/Modified site: allysine (Lys) #status predicted
F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental
F;263/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;364,1094/Modified site: 5-hydroxylysine (Lys) partial) #status experimental
F;364-099/Cleavage site: Gly-Ile (collagenase) #status experimental
F;1106/Binding site: carbohydrate (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A92516; MUID:85157600
A;Accession: A92516
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797;
                                                                                                                                                                                                                                                                                                                                              R;Bigi, F.; Alito, A.; Fisanotti, J.C.; Romano, M.I.; Cataldi, Infect. Immun. 63, 2581-2586, 1995
A;Title: Characterization of a novel Mycobacterium bovis secret A;Reference number: S60743; MUID:95310015
A;Accession: S60743
                                                                                                                                                              A;Cross-references: EMBL:248749
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted antigen P36/P34 precursor - Mycobacterium bovis
C;Species: Mycobacterium bovis
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S60743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homoloc;Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; F;1-23/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: structural component of extracellular fibrous polymer that maintains into C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology. C;Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hyc
                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-284 <BIG>
                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;168-1196/Region: helical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently
Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1091-1093/Region: cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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8; Conserv
      Conservative
                                 47.08;
47.48;
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Pred. No. 1.7e
4; Mismatches
      2;
                                 Score 47;
Pred. No.
Mismatches
                                 DB
42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7e+02;
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      Indels
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      ferredoxin--NADP+
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TPATPAPAAPTPATPAP

83

2 SPGTPAPAAEETMTTSP 18

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15

reductase

(EC

1.18.1.2) precursor -

Synechocystis sp.

(strain PCC

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, M.; Shen, M.; Vamathevan, J.J.; Lam, P.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M
Science 286, 1571-1577, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987 A;Accession: F70888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable pirG protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                               A; Map position:
                                                                                                                                                                                  A;Cross-references: GB:AE001939; GB:AE000513; NID:g6458563; PIDN:AAF10427.1; PID:g645
A;Experimental source: strain R1
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-375 <WHI>
                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                          A; Title: Genome sequence of A; Reference number: A75250; A; Accession: F75467
                                                                                                                                                                                                                                                                                                                                                                                                                              R;White,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Deinococc
C;Date: 03-Dec-1999
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A; Residues: 1-284 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: F70888
R; Cole, S.T.; Brosc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable lipoprotein – Deinococcus radiodurans (strain R1)
  Query Match
Best Local S
Matches
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 TSPGLTSPGLTDPALTSPG 118
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                                                                                                                                        DR0848
                                                                                                                                                                                                                                                                                                                                                                                                                            O.; Eisen, J.A.; Heidelberg, J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinococcus radiodurans
  Similarity 52.9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #sequence_revision
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                       47.0%;
52.9%;
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                                                                                                                                                                                                                                                                                                                    the radioresistant bacterium Deinococcus radiodurans MUID:20036896
Score
Pred.
2; Mis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-Dec-1999 #text_change 31-Mar-2000
                       47;
No.
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McDonald, L.; Utterback,
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42;
                  56;
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                                            Length 375;
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T.; Zalewski,
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A;Description: catalyzes electron transfer from reduced ferredoxin to NADP A;Pathway: photosynthesis
A;Pathway: photosynthesis
A;Note: FAD cofactor
C;Superfamily: ferredoxin--NADP+ reductase; cytochrome-b5 reductase homology
C;Keywords: electron transfer; FAD; flavoprotein; NADP; oxidoreductase; photosynthesis
F;1-112/Domain: signal sequence #status predicted <SIG>
F;1-113-413/Product: ferredoxin--NADP+ reductase #status predicted <MAT>
F;121-260/Domain: FAD binding #status predicted <FAD>
F;143-398/Domain: cytochrome-b5 reductase homology <CBR>
F;161-413/Domain: NADP binding #status predicted <NADP>
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A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76200
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; R.; Okmura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
Search completed: August 13, 2002, 08:30:05 Job time: 39 sec
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C;Complex: monomer
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P51012 rhodobacter
P08796 dictyosteli
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RN [4]  SEQUENCE FROM N.A., AND SEQUENCE OF N-TE RX MEDLINE-97390509; PubMed=9242611;  RA Sheridan J.P., Marsters S.A., Pitti R.M. RA Baldwin D., Ramakrishnan L., Gray C.L., RA Goddard A.D., Godowski P., Ashkenazi A.; RT "Control of TRAIL-induced apoptosis by a RT receptors."; RL Science 277:818-821(1997).  RN [5]	RP SEQUENCE FROM N.A., AND CHARACTERIZATIC RC 71SSUB=POTESKIN fibroblast; RX MEDLINE=97461602; PubMed=9314565; RA Degli-Esposti M.A., Smolak P.J., Walcza RA Dubose R.F., Goodwin R.G., Smith C.A.; RT Cloning and characterization of TRAIL, RT emerging TRAIL receptor family."; RI J. Exp. Med. 186:1165-1170(1997). RN [3] RN [3] RP SEQUENCE FROM N.A. SEQUENCE FROM N.A. PAN MEDLINE=97390508; PubMed=9242610; RA PAN PAN G., Ni J., Wei YF., Yu GL., Ger RT "An antagonist decoy receptor and a dea RT for TRAIL."; Schence 277:815-818(1997).	AC 014798; 014755; AC 014798; 014755; DT 16-0CT-2001 (Rel. 40, Last sequence update) DT 16-0CT-2001 (Rel. 41, Last annotation update) DT 16-MAR-2002 (Rel. 41, Last annotation update) DT 01-MAR-2002 (Rel. 41, Last annotation update) DE Tumor necrosis factor receptor superfamily member 10C p. DE receptor 1) (DCR1) (Decoy TRAIL receptor without death, DE related apoptosis-inducing ligand receptor 3) (TRAIL receptor ETRAIL/Apo-2L). DE (TYMPHOCYTE inhibitor of TRAIL) (Antagonist decoy receptor TRAIL/Apo-2L). GN TNFRSF10C OR DCR1 OR TRAILR3 OR TRID OR LIT. OS HOMO Sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutock Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hoo NCBI_TaxID-9606; RN [1] NEDLINE-97467318; PubMed-9325248; RA MEDLINE-97467318; PubMed-9325248; RA MacFarlane M., Almad M., Srinivasula S.M., Fernandes-Al RA Cohen G.M., Almamri E.S.; RT "Identification and molecular cloning of two novel receptors of the company of the company of the color of	34 44 44.0 889 1 ENV_SIVSP 35 44 44.0 1670 1 CA34_HUMAN 36 43.5 43.5 839 1 APB1_RAT 37 43 43.0 137 1 GILZ_MYCTU 40 43 43.0 261 1 LPRF_MYCTU 40 43 43.0 331 1 HXBAL_MOUSE 41 43 43.0 351 1 OPSP_CHUCK 42 43 43.0 351 1 OPSP_CHUCK 43 43 43.0 351 1 OPSP_CHUCK 44 43 43.0 351 1 OPSP_CHUCK 45 43 43.0 427 1 GSA_PASMU 46 43 43.0 432 1 GSA_VIBCH 47 48 48 49.0 432 1 GSA_VIBCH 48 49 49.0 492 1 GSA_VIBCH 49 49 49 49 49 49 49 49 49 49 49 49 49 4
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Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,

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"Characterization of two receptors FEBS Lett. 416:329-334(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              !igand): a new
!RAIL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Lymphocyte inhibitor of TRAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a cytoplasmic death domain and hence is not capable of inducing apoptosis. May protect cells against TRAIL mediated apotopsis by competing with TRAIL-R1 and R2 for binding to the ligand. SUBCELULAR LOCATION: Attached to the membrane by a GPI-anchor. TISSUE SPECIFICITY: Higher expression in normal tissues than in tumor cell lines. Highly expressed in peripheral blood lymphocytes, spleen, skeletal muscle, placenta, lung and heart. PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED. SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                           There are no rest
                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    death
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Best Local S
Matches 19
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O14763; O15531; O15508; O15517; O14720; O9BVEO;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 10B |
receptor 5) (TWF-related apoptosis-inducing ligand recreptor-2) (TRAIL-R2).
TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTN
                                                                                                                                                                                                                                                                                                                        cytotoxic signal from TRAIL.";
Curr. Biol. 7:693-696(1997).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 2
_HUMAN
                                                                                                                                                    Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., McKrantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.; "KILLER/DR5 is a DNA damage-inducible p53-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEDLILL Dey. Walczak H., Dey. Walczak H., Timour M.S., Pauch C.T
                                                                         MEDLINE-97390508; PubMed-9242610;
Pan G., Ni J., Wei Y.-F., Yu G.-I
"An antagonist decoy receptor and
                                                                                                                                                                                                                                                                                                                                                                                      SPLICING. MEDLINE-97431692;
 MacFarlane M.,
Cohen G.M., Alı
                   SEQUENCE FROM N.A. (SHORT ISOFORMEDLINE=97467318; PubMed=9325248;
                                                     Science
                                                                                                           SEQUENCE FROM
                                                                                                                                             gene.
                                                                                                                                                                                                  MEDLINE-97467719;
                                                                                                                                                                                                             TISSUE=Ovary;
                                                                                                                                                                                                                     SEQUENCE FROM N.A. (SHORT
                                                                                                                                                                                                                                            FEBS Lett.
                                                                                                                                                                                                                                                      Tschopp J.; "Characterization
                                                                                                                                                                                                                                                                                        MEDLINE=98039016;
                                                                                                                                                                                                                                                                                                   TISSUE-Liver,
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (LONG ISOFORM),
                                                                                                                                                                                                                                                                                                                                                                           Screaton G.R., Mongkolsapaya
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodwin R.G., Rauch C.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (LONG IS
TISSUE=Foreskin fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                McMichael A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                               "TRAIL-R2: a novel apoptosis-mediating EMBO J. 16:5386-5397(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97459925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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19; Conser
                                                       277:815-818(1997)
                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A. (LONG AND
                                                                                                                                                                                                                                                                         P.,
                                                                                                                                                                                                                                            416:329-334(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Degli-Esposti M.A., Johnson R.S., Simour M.S., Gerhart M.J., Schooley
                                                                                                                                 17:141-143(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                          N.A. (SHORT ISOFORM).
                                                                                                                                                                                                                                                                            Bodmer
           Ahmad
                                                                                                                                                                                                                                                                                                                                                                 Bell
                                                                                                                                                                                                  PubMed=9326928;
                                                                                                                                                                                                                                                        of two
                                                                                                                                                                                                                                                                                     Spleen;
PubMed=9373179;
                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9285725;
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                                (SHORT ISOFORM).
 M., Srinivasula
E.S.;
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and a
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Pred. No. 3.2e-06;
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                                                                           Gentz
death
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           3
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                                                                          R., Dixit V.M.;
domain-containing
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           Fernandes-Alnemri T.,
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y K.A.,
                                                                                                                                                                                                                                                                                                                                                        that transduces
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R., F
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                                                                                                                                                       death
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Smith C.A.,
                                                                                                                                                                            Hamilton
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Submitted [12]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98090092; PubMed-9430227; Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hohath receptor 5, a new member of the TNFR family, and DR4 in FADD-dependent apoptosis and activate the NF-kappaB pathway."; Immunity 7:821-830(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science
[9]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones E.Y., Screaton G.R.;
"Structure of the TRAIL-DR5 complex reveals mechanisms specificity in apoptotic initiation.";
Nat. Struct. Biol. 6:1048-1053(1999).
-I- FUNCTION: Receptor for the cytotoxic ligand TRAIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M. Kelley R.F., Ashkenazi A., de Vos A.M.;
"Triggering cell death: the crystal structure of Apo2L/TRAIL in complex with death receptor 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene in co
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MEDLINE-97390509; PubMed-9242611;
Sheridan J.P., Marsters S.A., Pitti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification and molecular cloning of two cytotoxic ligand TRAIL.";
J. Biol. Chem. 272:25417-25420(1997).
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Arai T., AKiyama Y., Okabe S., Saito K.,
"Genomic structure and mutation analyses
gene in colorectal carcinoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mongkolsapaya J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10542098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20017054;
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                                                                                                                                                            caspase 8 leading to subsequent activation of effector caspas that execute apoptotic death of the cell.

SUBUNIT: Homotrimer (Potential). Can interact with TRADD and SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM/TRICK2B (SHOWN AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICINA TISSUE SPECIFICITY: Widely expressed in adult and fetal tissu very highly expressed in tumor cell lines such as HeLa S3, K5 HL-60, SW480, A549 and G361; highly expressed in heart, periphilar the such as the content of the s
                                    very highly expressed in tumor cell lines such as HeIa S3, K5 HL-60, SW480, A549 and G361; highly expressed in heart, perip blood lymphocytes, liver, pancreas, speed, thymus, prostate, ovary, uterus, placenta, testis, esophagus, stomach and throu the intestinal tract; not detectable in brain.

INDUCTION: INFRSF10B is regulated by the tumor suppressor p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates apoptosis in a caspase-dependent manner. Can trigger the nuclear factor kappaB-pathway and can bind the cytoplasmic adapter molecule FADD/MORTI which engages initiator caspases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell 4:563-571(1999).
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, Zhang W., Wan '
ced (MAY-1999) t
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homolog
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       TNFRSF10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.M., Chen N., Xu X.-N.,
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   by the beaca
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ne tumor suppressor p53 cause of squamous cell
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SPLICING.
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InterPro; IPR001368; TNFR_C6.
Pfam; PF000531; death; 1.
Pfam; PF00020; TNFR_C6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50052; TNFR_NGFR_1; 2.
PROSITE; PS50052; TNFR_NGFR_2; 2.
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SIMILARITY: CONTAINS 1 LA-NGFR,
SIMILARITY: CONTAINS 1 DEATH DO
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603612; -.
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1D4V; 01-NOV-99.
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AF018657
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PS50050; TNFR_NGFR_2; 2.
Apoptosis; Transmembrane;
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to license@isb-sib.ch).
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1 DEATH DOMAIN.
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                Score 54;
Pred. No.
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POLY-GLY.
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Mismatches
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Best Local
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  HXB3_MOUSE STANDARD; PRT; 433 AA. P09026; P10285; Q61680; O1-NOV-1988 (Rel. 09, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Homeobox protein Hox-B3 (Hox-2.7) (MH-23). HOXB3 OR HOXB-3 OR HOX-2.7.
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P04294;
20-MAR-1987
                                                                                                                                                                                                               MOUSE
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PIR; C30083; C30083.

InterPro; IPR001616; Herpes_alk_exo.

Pfam; PF01771; Herpes_alk_exo; 1.

PRINTS; PR0924; ALKEXNUCLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=88274327; PubMed=2839594;

McGeoch D.J., Dalrymple M.A., Dav

McGeoch D.J., Scott J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-86205244; PubMed-3010237; McGeoch D.J., Dolan A., Frame M.C.; "DNA sequence of the region in the genome of herpes simplex virus type 1 containing the exonuclease gene and neighbouring genes."; Nucleic Acids Res. 14:3435-3448(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McNab D., Perry L.J., Scott J.E., Taylor P.; "The complete DNA sequence of the long unique region in the genom herpes simplex virus type 1."; J. Gen. Virol. 69:1531-1574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
SEQUENCE
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626 AA; 6
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67508 MW; 7B86C941A0105035
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EMBL; X66177; CAA46951.1; -. EMBL; U02278; AAB60496.1; -. EMBL; M18168; AAA37840.1; -. PIR; S20963; S20963. PIR; C29585; C29585. HSSP; P02833; ISAN.
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InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                            PRINTS; PR00025; ANTENNAPEDIA. PRINTS; PR00024; HOMEOBOX. SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "New murine homeoboxes: structure, chromosomal assignment, differential expression in adult erythropoiesis."; DNA 6:409-418(1987).
                                                                                          PROSITE; PS00027; PROSITE; PS00032; PROSITE; PS50071;
                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 181-265 FROM N.A. MEDLINE=89091992; PubMed=2463210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of the murine Hox-2.7 gene: conserved alt transcripts with differential distributions in the the potential for shared regulatory regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sham M.H., Hunt P., Nonc
Boncinelli E., Krumlauf
                                                                   Transcription
                                                                                                                                                                                              TRANSFAC; T01724; -. MGD; MGI:96184; Hoxb3
                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krumlauf R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graham A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95196953; PubMed=7890121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=92258392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of a murine homeo 
Drosophila Deformed gene.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88054465;
                                                                                                                                                                                                                                                                                                                                   European Bloinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5'-sequence of the murine Hox-b3 (Hox-2.7) gene ain multiple transcription-regulatory elements.", J. Biochem. 26:1403-1409(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. 11:1825-1836(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P., Arman E., Czosnek H., Ruc
murine homeoboxes: structure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W.M., Taylor G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF 152-361 FROM N.A.
88054465; PubMed=2890503;
                                                                               DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papalopulu N., Lorimer J.,
 129
154
191
113
113
119
                                                                   regulation.
                                                                                          номеовох_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=1582411;
                                                                                                      ANTENNAPEDIA;
                                                                                                                 HOMEOBOX_1; 1.
134
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                                                                               protein; Nuclear
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                                                         HEXAPEPTIDE
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                                                                                                                                                                                                                                                                                                                                                There are no restrictions
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                                                                                                                                                                                                                                                                                                                            Usage
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RESULT
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Best Local
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Dev. Gro
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                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute1eosu
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q919M5;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frizzled homologs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FZD1_XENLA
                                use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20424135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Frizzled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MAR-2002 (Rel. 41, Created)

-MAR-2002 (Rel. 41, Last sequence update)

-MAR-2002 (Rel. 41, Last annotation update)

-izzled 1 precursor (Frizzled-1) (Fz-1) (Xfz1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w
         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial infied and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                   pronephros and otic vesicles.

DEVELOPMENTAL STAGE: Abundant in unfertilized eggs. Not detection late gastrula or early neurula stages. Expressed in mid-new stages and maintained through tadpole stages.

DOMAIN: Lys-Thr.X-X-X-Trp motif is involved in the activation boundary.
                                                                                                                                                                                                                                                                                                                                                                           are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishvelled protesins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of whit target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Whit-mediated inactivation of GSK-3 kinase. Both pathways seem
                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein TISSUE SPECIFICITY: In the embryo, expressed in
                                                                                                           SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
                                                                                                                                        similarity).
SIMILARITY: BELONGS
                                                                                                                                                                           DOMAIN:
                                                                                                                                                                                                                                                                                                                  information during tissue morphogenesis tissues. Binds to Wnt8.
                                                                                                                                                                                                                                                                                                                                 to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor
                                                                                                                              RECEPTORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGSPPPSAAPTSTTS
                                                                                                                                                                       Wnt/beta-catenin signaling pathway AIN: The fz domain is involved in bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .D., Hallagan S.E., McGrew L.L., Miller J.R., Moon R.T.; ternal Xenopus beta-catenin signaling pathway, activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433
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duces goosecoid in a cell non-autonomous
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                                                                                                                                           FAMILY
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D -> N (IN REF. 4).

LC -> FV (IN REF. 3).

S -> L (IN REF. 3).

GAYGTPTMQGSPVYVGGGGY -> I

VAT (IN REF. 3).
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   (See
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binding with Wnt
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                                                                                                                                          G-PROTEIN COUPLED
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                                                                                                                                                                                                                                                                                                                                    differentiated
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                                                                                                                                                                                                                                                                                    heart,
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50038; FZ; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
Multigene family; G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01392; Fz; 1.
Pfam; PF01534; Frizzled; 1.
                                                                                                                                                                                                                                                                                                                                                           MOUSE
SX13_MOUSE
                                                           "High expression of the embryonic development.";
                                                                                                                          TISSUE=Embryo;
MEDLINE=98083175;
                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                            Mus
                                                                                                                                                                                                                                                          SOX-13 protein.
SOX13 OR SOX-13.
                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 01-MAR-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00489; FRIZZ SMART; SM00063; FRI; 1
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SEQUENCE FROM
TISSUE-Embryo;
                                                                                           Roose J., Korver W.,
Lamers W., Clevers H.
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                            01-JUN-1994
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                                               Nucleic Acids
                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                            musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSPGTPAPAAEETMTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity
9; Conser
                                                                                                                                                              FROM
                                     development.";
rids Res. 26:469-476(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000024;
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               z
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                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRIZZLED.
                                                                                                      PubMed=9421502;
ra Oving E., Wilson A.,
                                                                                                                                                                                                                                                                                          29,
39,
41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                             Rodentia;
             AND
                                                                                                                                                                                                                         Chordata;
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52.9%;
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6 (POTENTIAL).
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Pred. No.
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N-LINKED (GLCNAC. . .) (P
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4 (POTENTIAL)
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3 (POTENTIAL).
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2 (POTENTIAL)
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33;
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   Eukaryota;
Mammalia; E
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                                                                             Collagen alpha
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development.";
Nucleic Acids Res. 21:744-744(1993).
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Kido S., Hiraoka 1
                                          Homo sapiens
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Wright E.M., Snop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: BINDS TO THE SEQUENCE 5'-AACAAT-3'.
SUBCELIULAR LOCATION: NUCLEAR (POCENTIAL).
ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE)
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Q05066; 1HRY.
MGI:98361; SOx13
rPro; IPR000910;
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ning and characterization
208:201-206(1998).
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8; Conservative
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Eutheria;
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PubMed=8441686;
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(IN ISOFORM 2).
Craniata; Vertebrata; Catarrhini; Hominidae
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T -> TN (IN REF. 2).
2 -> QQ (IN REF. 2).
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of mouse mSox13 cDNA.
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   Hominidae;
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REVISIONS.
Seyer J.M.
Submitted
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[9]
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Biochemistry 17:3404-3411(1978).
[6]
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                                                                                                                               SEQUENCE OF 1065-1466 FROM N.A. MEDLINE-85087944; PubMed-6096827; Loidl H.R., Brinker J.M., May M.,
                                                                                                                                                                         REVISION TO 1184.

MEDLINE-89098346; PubMed-3211760;

Molyneux K., Dalgleish R.;

"Human type III collagen 'variant
Nucleic Acids Res. 16:11833-11833
                                                                                                                                                                                                                                    SEQUENCE OF 950-1466 FROM N.A. MEDLINE-88189827; Pubmed-3357782; Mankoo B.S., Dalgleish R.; Mankoo B.S., Dalgleish R.; CDlagen: cDN "Human pro alpha 1(III) collagen: cDN Nucleic Acids Res. 16:2337-2337(1988)
                                                                                                                                                                                                                                                                                                Seyer J.M., Mainardi C., Kang A.H.; 
"Covalent structure of collagen: amm (III)-CB5 from type III collagen of 
Biochemistry 19:1583-1589(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of cDNA clones coding chain of human type III procollage and conse Biochem. J. 260:509-516(1989).
                  1(III)-CB9 from
Biochemistry 20:
                                                          SEQUENCE OF 965-12
MEDLINE-81208139;
                                                                                                   procollagen."
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of human liver.";
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SEQUENCE OF
                                       Seyer J.M., Kang A.H
"Covalent structure
                                                                                          Nucleic
                                                                                                             Rosenbloom J., Myers
"Molecular cloning an
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 728-964.
MEDLINE=80198282; Pu
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=79000343;
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MEDLINE=77134724; PubMed=557335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89350838; PubMed=2764886; Ala-Kokko L., Kontusaari S., Bald
                                                                                  [10]
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collagen 'variant' is a
es. 16:11833-11833(1988)
                   type III collag
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                                                 A.H.;
                                                           PubMed=7016180;
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                                               WARLANY EUSTAY AND YORK MEDILINE-94016385; PubMed-8411057; Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M. "The substitution of glycine 661 by arginine in type III coll produces mutant molecules with different thermal stabilities produces matant molecules with different thermal stabilities produces mutant molecules with different thermal stabilities
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MEDLINE-88303360; PubMed-3405773;
Toman D., Ricca G., de Crombruggi
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MEDLINE-91045136; PubMed-2235526;
Kleinert C., Tromp G.,
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MEDLINE-89378752;
Benson-Chanda V.,
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Chu M.-L., Weil D., de Wet W.J., Bernard M.P., S
"Isolation of cDNA and genomic clones encoding b
(III) collagen. Partial characterization of the
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MEDLINE=91056145; PubMed=2243125;
VARIANT
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with aortic aneurysms.",
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of human prepro alpha 1(III) collagen.";
Nucleic Acids Res. 16:7201-7201(1988).
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17804; PubMed-3754462;
Dalgleish R., Kluve-Beckerman
P., Brantly M., Crystal R.G.;
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"A single base mutation that substitutes serine for glycine
the alpha I (III) chain of type III procollagen exposes an a
and causes Ehlers-Danlos syndrome IV.";
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patient with Ehlers-Danlos syndrome
J. Med. Genet. 28:458-463(1991).
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                                                                                                                                                                                                                                                                                                                                                         "Attenuation of virulence by tuberculosis erp gene."; Science 282:759-762(1998).
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Lim E.M., Rauzier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishai W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dentification of Mycobacterium tuberculosis DNA ported proteins by using phoA gene fusions."; Bacteriol. 177:59-65(1995).
                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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Q55318; P74364;
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01-NOV-1997 (Rel. :
16-OCT-2001 (Rel. :
                                                                                                                                                                                                                                                                          Keneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yanada M., Yasuda M., Tabata S.; Yamada M., Yasuda M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and asygnament of potential protein-coding regions.";
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          SWISS-PROT entry is copyright. It is produced the Empty is Institute of Bioinformatics and the Empty is Institute. There are no restrained as its content in the content in
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                                                                                                                                                                                                      MEDLINE-80026027; PubMed-488907; Dewes H., Fietzek P.P., Kuhn K.; The covalent structure of calf skin acid sequence of the cyanogen bromide (positions 223-402).";
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 SEQUENCE OF
                                   Hoppe-Seyler's
                                                       amino acid sequence of the cyanogen bromide peptide (positions 403-551).";
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NADP (RIBOSE PART)
E -> K (IN REF. 1).
D -> S (IN REF. 1).
QHRV -> STGL (IN REF. 1).
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FF33709639F0CAA8 CRC64;
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Mus musculus (Mouse).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Rc
NCBI_TaxID=10090;
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CARBOHYD
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SEQUENCE
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                                                        CA13_MOUSE STANDARD; PRT; 1464 AA P08121; Q61429; Q9CRN7; 01-AUG-1988 (Rel. 08, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Collagen alpha 1(III) chain precursor.
                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=80026031; PubMed=488911;
Allmann H., Fietzek P.P., Glanville R.W., Kuhn K.;
"The covalent structure of calf skin type III collagen.
acid sequence of the carboxyterminal cyanogen bromide pe
1(III)CB9B (positions 928-1028).;
Hoppe-Seyler's Z. Physiol. Chem. 360:861-868(1979).
-i- FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=80026030; PubMed=488910; Dewes H., Fietzek P.P., Kuhn K.; The covalent structure of calf skin acid sequence of the cyanogen bromide (position 789-927).";
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Lang H., Glanville R.W., Fietzek P.P., Kuhn K.;
"The covalent structure of calf skin type III collagen. IV. Tacid sequence of the cyanogen bromide peptide alpha 1(III)CB5 (positions 552-788).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01391; Collagen; 17. PROSITE; PS01208; VWFC; PARTIAL.
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InterPro; IPR001007; VWFC
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SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS AI
LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE
ALSO CROSS-LINKED VIA HYDROXYLYSINES.
PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
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Pred. No. 85;
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O-LINKED (GAL.
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            Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue;
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DCCURS IN MOST SOFT CONNECTIVE TISSUES
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            Muridae;
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            Murinae;
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KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Schai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Tanaka M., Marchional T., Mang K.H., Weitz C., Whittaker C., Wilming L., Wang K.H., Weitz C., Whittaker C., Whittaker C., Wilming L., Wang K.H., Weitz C., Whittaker C., Wang K.H., Weitz C., Whittaker C., Wang K.H., Weitz C., W
collagen mrNas.";
Biophys. Acta 1089:241-243(1991).
Biochim. Biophys. Acta 1089:241-243(1991).
-I- FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONN ALONG WITH TYPE I COLLAGEN.
-I- SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. 1
LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS.
                                                                                                                                                                        This
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Metsaeranta M., Toman D., de Crombrugghe
"Specific hybridization probes for mouse
                                                          use by non-profit institute modified and this statement entities requires a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Embryonic MEDLINE=21085660; PubMed=11217851;
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SEQUENCE FROM N.A.
STRAIN-C57BL X DBA; TISSUE-Embryo;
MEDLINE-95011609; PubMed-7926795;
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"The mouse type-III procollagen-encoding gene: genomic cloning
                                        tities requires a license agreement (See send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem.
                                                                                                                                                                                                               PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. O-LINKED GLYCAN CONSISTS OF GLC-CAL DISACCHARIDE (BY SIMILARITY: CONTAINS 1 VWFC DOMAIN.
                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                         ALSO CROSS-LINKED VIA HYDROXYLYSINES
                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lete DNA sequence."
147:161-168(1994).
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  CAA36279
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260:3773-3777(1985).
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PubMed=3443309;
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Best Local
MEDLINE-20345099; PubMed-10884428; Santamarina-Fojo S., Peterson K.M., Knapper C.L., Qi Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Haudenschild C.C., Prades C., Chimini G., Blackmon E Francois T.L., Duverger N., Rubin E.M., Rosier M., D Fredrickson D.S., Brewer H.B. JT.; "Complete genomic sequence of the human ABCAl gene: human and mouse ATP-binding cassette A promoter.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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ProDom; PD002078; Fib_collagen_C;
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Deleuze J.-F., Brewer H.B., Duverger N., Denef
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van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,

van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,

Loubser O., Ouelette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,

Sensen C.W., Scherer S., Mott S., Denis M., Martindale D.,

Sensen C.W., Scherer S., Mott S., Pimstone S., Kastelein J.J.P.,
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Collins J.A., van Dam M., Molhuizen H.O.F., Loubser O.,
Ouelette B.F.F., Sensen C.W., Fichter K., Mott S., Denis M.,
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22:336-345(1999).
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VARIANTS TD ASN-1289 AND HIS-1800.
WARIANTS TD ASN-1289 AND HIS-1800.
MEDLINE-20171564; PubMed-10706591;
Brousseau M.E., Schaefer E.J., Dupuis J., Eustace E
Brousseau M.E., Schaefer E.J., Thurston L.M., Fit
Van Eerdewegh P., Goldkamp A.L., Thurston L.M., Fit
Yasek-McKenna D., O'Neill G., Eberhart G.P., Weiff(
Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z
Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z
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MEDLLINE=20396633; PubMed=10938021;
Wang J., Burnett J.R., Near S., Young K.,
Connelly P.W., Harris S.B., Hegele R.A.;
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Suda T., Ceska
            MEDLINE=21138379;
Clee S.M., Zwinder
Molhuizen H.O.F.,
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MEDLINE-21369433; PubMed-11476965;
Huang W., Moriyama K., Koga T., Hua H., Aç
Mawatari K., Imamura T., Eto T., Kawamura
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MEDLINE-21157002; PubMed-11257260;
Bertolini S., Piscolotta L., Seri M., Cuss
Calabresi L., Franceschini G., Ravazzolo
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J. Lipid Res. 41:433-441(2000).
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Zwarts K.Y., Collins J.A., Roelants R.,
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Brooks-Wilson A., Molhuizen H.O.F., Frob
                                                                                                                    "Novel mutations in ABCA1 gene in disease and familial high density
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MEDLINE=21369429; Pu
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Andrikovics H., Boettcher
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                                                                  LYS-219;
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            Zwinderman A.H.,
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r A., Hubacek
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n L.M., FitzGerald
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DeSouich C.
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M., Teramoto T., Sasaki J.;
patients with Tangier
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ek J., A
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P51012;

T 01-OCT-1996 (Rel. 34, Created)
T 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, East annotation update)
DE Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (Per Ribulose-phosphate 3-epimerase (EC 5.1.3.1)
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"Common genet
lipoprotein ]
       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 11166;
STRAIN-ATCC 11167
Larimer F.W., Lu T. -Y.S., Buley D.N
Submitted (OCT-1997) to the EMBL/GG
-!- CATALYTIC ACTIVITY: D-ribulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression and functional analyses of novel mutations of ATP-binding cassette transporter-1 in japanese patients with high-density lipoprotein deficiency.";
Biochem. Biophys. Res. Commun. 290:713-721(2002).
-I- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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Ishihara M., Sakane N., Zhang Z., Tsujli K., Ma
Matsuura F., Ishigami M., Sakai N., Hiraoka H.,
Wellington C., Yoshida Y., Misugi S., Hayden M.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
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                                                                                                                                                                                                                            SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                        PATHWAY: CALVIN CYCLE
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                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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.he EMBL/GenBank/DDBJ databases
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Best Local :
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MEDLINE=89251561; PubMed=2721485;

Stadler J., Keenan T.W., Bauer G.,

"The contact site A glycoprotein og a phospholipid anchor of a novel t
                                                                                                                                                       Kamboj R.K., Wong L.M., Lam T.Y.,
"Mapping of a cell-binding domain
of Dictyostelium discoideum.";
J. Cell Biol. 107:1835-1843(1988).
                                                                                                                                                                                                                                                                                                                                    Wong L.M., Siu C.-H.;
"Cloning of cDNA for
discoideum.";
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HSSP; Q43843; IRPX.
InterPro; IPR000056; Ribul_P_3_epim.
Pfam; PF00834; Ribul_P_3_epim; 1.
PROSITE; PS01085; RIBUL_P_3_EPIMER_1; 1.
PROSITE; PS01086; RIBUL_P_3_EPIMER_2; FALSE_NEG.
ISOMETASE; Carbohydrate metabolism; Calvin cycle
SEQUENCE 228 AA; 23878 MW; FCD392695BCD396B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92406924; PubMed-1326559;
Desbarats L., Lam T.Y., Wong L.M., Siu C.H.;
"Identification of a unique cAMP-response element encoding the cell adhesion molecule gp80 in Dictyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-AX2
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                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 20-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A MEDLINE=89105362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noegel A., Gerisch G., Stadler J., Westphal M.; "Complete sequence and transcript regulation of protein from aggregating Dictyostelium cells."; EMBO J. 5:1473-1476(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Molecular mechanisms
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                                                                                                                                                                                                                                                                                                                                                                                     C.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      267:19655-19664(1992).
                                                                                                                                                                                                                                                  PubMed=3182938;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tein precursor (CSA) (Membrane-associated
 (Cell adhesion molecule GP80).
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of c
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cell-cell interaction
                     novel type.";
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Pred. No. 21;
2; Mismatches
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                                       of Dictyostelium
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Dictyostelium
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RESULT 15
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ID 2151_CHICK
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DT 30-MAY-2000
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Best Local
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EMBL; M36545; AAA3212.1; -.
EMBL; X66483; CAA47110.1; -.
PIR; A23951; A23951.
PIR; A26310; A26310.
PIR; A31643; A31643.
PIR; S22066; S22066.
PIR; A44100; A44100.
DictyDb; DD02005; csaA.
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LIPID
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002909; IPT_TIG.
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PTM: ACYLATED, PHOSPHORYLATED ON SERINE AND N-GLYCOSYLATED WITH
TWO TYPES OF OLIGOSACCHARIDE CHAINS.

MISCELLANEOUS: THE EXPRESSION OF THIS STRINGENTLY REGULATED
PROTEIN DURING CELL DEVELOPMENT IS MEDIATED THROUGH CELL-SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O J. 8:371-377(1989).

FUNCTION: THIS CELL-SURFACE GLYCOPROTEIN MEDIATES CELL-CELL BINDING VIA HOMOPHILIC INTERACTION.

SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHO THAT CONTAINS A PHOSPHOCERAMIDE MOIETY, SUCH ANCHOR MEDIATES FAST AND LONG PERSISTENCE CELL ADHESION OF THE PROTEIN.

DEVELOPMENTAL STAGE: RESTRICTED TO THE AGGREGATION STAGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAMP
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9; Conserv
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                                                                   STANDARD;
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V -> G (IN REF. 1).
; 96AlC7CF42FEC096 CRC6
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REMOVED IN MATURE FORM (POT
GLOBULAR (POTENTIAL).
PRO-RICH (HINGE STRUCTURE).
2 X 8 AA REPEATS, PRO-RICH.
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MEDLINE=96003919; PubMed=7575457;
Schulz T.C., Hopwood B., Rathjen P.D., Wells J.

"An unusual arrangement of 13 zinc fingers in t
213.";
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SMART; SM00355; ZDF_C2H2; 13.

PROSITE; PS50097; BTB; PARTIAL.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1

Transcription regulation; DNA-binding;
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Zinc finger protein 151 (Zinc finger protein Z13) (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restricted the statement of the statement of the swiss of the statement of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 311:219-224(1995).
-i- SUBCELLULAR LOCATION: Nuclear (Potential).
-i- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U14555; AAA21556.1; -. HSSP; P08047; 1SP2.
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InterPro; IPR000822; Znf-C2H2.
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SPSRPQPAESEVGNSSPG
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9; Conserv
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50.0%;
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Pred. No.
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the vertebrate
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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49.5
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mac:*
8: sp_organell:
9: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
12: sp_virus:*
13: sp_verteb:
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Match
          BLOSUM62
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Q91j64 arabidojsis
Q9wrt5 macaca mula
Q9j219 macaca mula
Q23635 caenorhabdi
Q9k4c4 streptomyce
P91859 caenorhabdi
Q9k4c4 streptomyce
Q91852 mus musculu
Q9gy9 leishmania
Q914x1 streptomyce
Q61769 mus musculu
Q9gy9 human herpe
Q68979 human herpe
Q68978 human herpe
Q9qnf4 human herpe
Q9qnf4 human herpe
Q9qnf4 human herpe
Q9qnf4 human serpe
Q9qnf4 human gall
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Q9HA18	Q9Y6I3	Q9NW45	Q9Z4V4	Q9BU21	Q9RW21	Q9LIX7	Q9VEC7	040942	P88955	Q9HEI9	Q62255	Q9BXA9	Q9UGH1	Q9U9K7	Q93336	Q9JIK1	001699	Q9U9K6	017866	Q9Y2D9	Q922L3	Q9H6L5	Q96V97	083835	Q99N63	Q99CW8	P78429	088339
homo		Q9nw45 homo sapien	Q9z4v4 streptomyce	Q9bu21 homo sapien		Q9lix7 oryza sativ	Q9vec7 drosophila	kaposi's	u	neuro	5 mus	homo	Q9ughl homo sapien	Q9u9k7 caenorhabdi	()	$\vdash$		Q9u9k6 caenorhabdi	caen	homo	3 mus		orpinomyces	O83835 treponema p	mesocr	Q99cw8 bovine herp	homo sap	O88339 rattus norv

## ALIGNMENTS

DR DR DR SQ	RA RT	R R R R R R N N O O O O O O	RESULT Q9LJ64 ID Q AC Q DT 0 DT 0
DNA Res. 7:217-221(2000).  EMBL; AP000735; BAB01698.1;  InterPro; IPR001226; Flavodoxin.  InterPro; IPR003592; LRR_Out.  InterPro; IPR003592; LRR_Out.  InterPro; IPR003592; Pistil_extensin.  InterPro; IPR002965; P_rich_extensn.  PRINTS; PR01217; PRICHEXTENSN.  PRINTS; PR01218; PSTLEXTENSIN.  SMART; SM00370; LRR; 5.  PROSITE; PS00201; FLAVODOXIN; UNKNOWN_1.  PROSITE; PS00201; FLAVODOXIN; UNKNOWN_1.	SEQUENCE FROM N.A. STRAIN-COLUMBIA; MEDLINE-20363099; PubMed=10907853; Makamura Y.; Nakamura Y.; "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, TAC and BAC clones.";	Arabidopsis thaliana (Mouse-ear cress). Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TAXID=3702; [1] SEQUENCE FROM N.A. STRAIN-COLUMBIA; STRAIN-COLUMBIA; Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.	LT 1 64 64 69LJ64 PRELIMINARY; PRT; 956 AA. 09LJ64; PRESIMENT PRT; 956 AA. 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
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Q9WRT5;
01-NOV-1999
                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Gammaherpesvirinae; Rhadinovirus. NCBI_TaxID=119193;
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InterPro; IPR001064; Crystallin.
Pfam; PF00716; Peptidase_S21; 1.
PRINTS; PR00236; HSVCAPSIDP40.
PROSITE; PR00235; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 536 AA; 58375 MW; E9C3DADB9AD043C0 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searles R.P., Bergquam E.P., submitted (JUN-2000) to the I EMBL; AF083501; AAD21343.1; HSSP; P16753; 1WPO.
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MEDLINE-99174001: PubMed=10074154;

Searles R.P., Bergquam E.P., Axthelm M.K., Wong S.W.;

Searles and genomic analysis of a rhesus macaque rhadinovirus similarity to Kaposi's sarcoma-associated Herpesvirus/Human herpesvirus 8.";
                                                                                                                 SEQUENCE FROM N.A. STRAIN-MACACA MULATTA RHADINOVIRUS MEDLINE=20173730; PubMed=10708456;
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Viruses; dsDNA viruses, no RNA stage;
Gammaherpesvirinae; Rhadinovirus.
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01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
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                                                     Alexander L., I
Desrosiers R.C
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rhesus monkey
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                                                                                        A., Auerbach M.R.,
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Eukaryota; Metazoa; Nema
Rhabditidae; Peloderinae
NCBI_TaxID=6239;
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Q23635;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Wortimore B., O'Callaghan
Lightning J., Percy C., Rifken L., Roopra A., Saunders D., Shownke
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III o:
elegans.";
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InterPro; IPR001847; Assemblin.
InterPro; IPR001064; Crystallin.
Pfam; PF00716; Peptidase_S21; 1.
PRINTS; PR00236; HSVCAPSIDP40.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
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J. Virol. 74:3388-3398(2000).
EMBL; AF210726; AAF59995.1; -.
HSSP; P16753; 1MPO.
                                                                                                                  "The sequence of C. elegans co
submitted (APR-1995) to the EL
EMBL; U2318; ARC48204.1; -
SEQUENCE 801 AA; 77123 MW;
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
ZK84.1 PROTEIN.
                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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MEDLINE-94150718;
                                                                                                                                                                   Kirsten J.;
                                                                                                                                                                                                                      Nature 368:32-38(1994).
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F32A7.5.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato.
Rhabditidae; Peloderinae;
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01-MAY-1997
01-MAY-1997
01-DEC-2001
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Bacteria; Firmicutes; Actinobacteria; Actinobacterida Actinomycetales; Streptomycineae; Streptomycetaceae; ACBI_TaxID=1902;
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"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL359152; CAB94558.1; -.
investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z83107; CAB054981; -.
InterPro; IPR001360; Glyco_hydro_1.
PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.
SEQUENCE 878 AA; 92237 MW; E7AF7851A88CCCOE CRC64;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A MEDLINE=99069613;
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Bentley S.D., Parkhill J.,
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                       O9GY99 PRELIMITATION, O9GY99;
O1-O2T-2001 (TrEMBLrel. 16, Cr
O1-DEC-2001 (TrEMBLrel. 18, Lager of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Mus musculus (Mouse).
Arvota; Metazoa; Chordata;
Aberia; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              088852
                                             Murphy L.,
Oliver K.;
                                                                                                             SEQUENCE FROM N.A.
STRAIN=FRIEDLIN;
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           Submitted
                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                        LM12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                          NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                  Leishmania
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family.";
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nes 10; Conserv
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                                                                                                                                                                                                                                                            major.
Euglenozoa;
                                                                           Quail M.,
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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h O., Mehraein Y.,
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       EMBL/GenBank/DDBJ
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Sciurognathi; Muridae;
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Q9L4X1;
01-OCT-2000
Q61769
Q61769;
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Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF02801; ketoacyl-synt_C; 1.
Pfam; PF00975; Thioesterase; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brautaset T., Sekurova O.N., Sletta H., Ellingsen T.E., Strovalla S., Zotchev S.B.;
"Biosynthesis of the polyene antifungal antibiotic nystatin Streptomyces noursei APCC 11455: analysis of the gene cluste deduction of the biosynthetic pathway.";
Chem. Biol. 7:395-403(2000).
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InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR000794; Ketoacyl-synt.
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR001031; Thioesterase.
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InterPro; IPR002202; WW.
Pfam; PF00397; WW; 1.
SMART; SM00456; WW; 1.
PROSITE; PS00066; HMG_COA_REDUCTASE_1; UNKNOWN_1.
PROSITE; PS00066; HMG_COAIN_2; 1.
SEQUENCE 989 AA; 110918 MW; 8F83B79AE6607D45
                                                                                                                                                                                                                                                                                                                                        Phosphopantetheine; SEQUENCE 2066 AA;
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MEDLINE=20334850; PubMed=10873841;
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J. Cell Sci. 109:143-153(1996).
EMBL; X82786; CAA58026.1; -.
MGD; MGI:106035; MX167.
InterPro; IPR000253; FHA_domain.
Pfam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
SEQUENCE 2938 AA; 324425 MW;
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01-NOV-1996
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KI-67 PROTEIN.
MKI67 OR KI-67.
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Q68979;
           InterPro; IPR001616; Herpes_alk_exo.
Pfam; PF01771; Herpes_alk_exo; 1.
PRINTS; PR00924; ALKEXNUCLASE.
                                          and type 2 alkaline exonucleases J. virol. 57:1023-1036(1986). EMBL; K02022; AAA45772.1; -.
                                                                                                                                          transcripts encoding alkaline exonuclease and a 50,000-dalton tentatively identified as a capsid protein."; J. Virol. 48:591-603(1983).
                                                                                                                                                                                                                                         human herpesvirus 1.
Viruses; dsDNA viruses,
Alphaherpesvirinae; Simman (CBI_TaxID=10298;
                                                                                                                                                                                                                                                                                                                                                                                                          1863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96431717; PubMed=8834799;
Starborg M., Gell K., Brundell E., Hoog C.;
"The murine K1-67 cell proliferation antigen accumulates in
nucleolar and heterochromatic regions of interphase cells ar
periphery of the mitotic chromosomes in a process essential
                                                                                      Draper K.G., Wagner E.K.;
                                                                                                           SEQUENCE FROM N.A. MEDLINE=86144016;
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MEDLINE-96431717; PubMed-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                          "High-resolution characterization of herpes simplex
                                                                                                                                                                                                            SEQUENCE OF 1-63 FROM N.A. MEDLINE=84036396; PubMed=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                          "Characterization of the genes encoding
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Q68978;
01-NOV-1996
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Phigh-resolution characterization of herpes simplex virus type 1

"High-resolution characterization of herpes simplex virus type 1
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SEQUENCE OF 1-189 FROM N.A.
MEDLINE=84036396; PubMed=6313961;
Draper K.G., Banks L.,
                                                                                                 human herpesvirus 1.
Viruses; dsDNA viruses,
Alphaherpesvirinae; Simp
NCBI_TaxID=10298;
                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, ALKALINE DEOXYRIBONUCLEASE.
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Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10298;
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SEQUENCE
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Pfam; PF01771; Herpes_alk_exo; 1.
PRINTS; PR00924; ALKEXNUCLASE.
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J. Virol. 57:1023-1036(1986).
EMBL; K02022; AAA45771.1; -.
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MEDLINE-86144016; Publ
Draper K.G., Devi-Rao
Wagner E.K.;
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-Rao G., Costa R
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EMBL: AB009266; BAA84005.2; -.
Interpro; IPR001616; Herpes_alk_exo.
Pfam; PF01771; Herpes_alk_exo.
PRINTS; PR00924; ALKENNUCLASE.
SEQUENCE 626 AA; 67484 MW; 88183DEAB9B0DA7.
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Analysis of nucleotide sequence variations:
types 1 and 2, and varicella-zoster virus.";
Acta Virol. 42.401-407(1998).
EMBL; AB009265; BARB40004.2;
InterPro; IPR001616; Herpes_alk_exo.
Pfam; Pf01771; Herpes_alk_exo;
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01-JUN-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
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           Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Pseudomonas
                                                        TATE PROTEIN.
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RC STRAIN=ZOBELL ATCC14405;
RX MEDLINE=21101859; PubMed=11160097;
RA Heikkilae M.P., Honisch U., Wunsch P., Zumft W.G.;
RT. "Role of the Tat transport system in nitrous oxide reductase
RT translocation and cytochrome cdl biosyntheis in Pseudomonas
RT stutzeri.";
RI J. Bacteriol. 183:1663-1671(2001).
DR EMBL; AJ299712; CAC29148.1; -.
DR InterPro; IPR003998; TatB.
DR FRINTS; PR01506; TATBDROTEIN.
SQ SEQUENCE 139 AA; 14772 MW; 5F82C4A9F09195AF CRC64;
SQ SEQUENCE 139 AA; 14772 MW; 5F82C4A9F09195AF CRC64;

Query Match
Best Local Similarity 58.8%; Pred. No. 15;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QV 2 SPGTPAPAAEETMTTSP 18
Ull | | | | | | | |
Db 117 SPAVPAPAAEETMTTSP 133

Search completed: August 13, 2002, 08:37:08

Job time: 392 sec
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Run 8 ھ

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Result
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US-09-141-212-4	US-09-141-212-2	US-09-378-255-6	US-09-225-170-12	US-08-916-917-12	US-09-103-429A-4	US-09-103-429A-3	US-09-086-483A-2	US-09-129-888-2	US-08-569-063C-15	US-08-609-443B-15	US-08-804-227C-2	US-09-189-462-4	US-08-979-608A-5	US-09-439-897-2	US-09-167-364-24	US-08-399-889-24	US-08-234-265A-11
Sequence 4, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 12, Appl		Sequence 4, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 15, Appl	Sequence 15, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 24, Appl	Sequence 24, Appl	Sequence 11, Appl

## ALIGNMENTS

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US-09-006-353A-2
                                                                                              ; SEQUENCE CHARACTERISTICS:
; LENGTH: 259 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-006-353A-2
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                                                                                                                                                                                                           TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TUMOR NECROSIS NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/006,353A FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: BROOKES, ANDERS A REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WEI, YING-FEI APPLICANT: YU, GUO-LIANG APPLICANT: GENTZ, REINER APPLICANT: RUBEN, STEVEN
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Best Local Similarity
Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/061,334
EARLIER FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 299
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08883036A Patent No. 6072047
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APPLICANT: McDonnell, Peter C.
APPLICANT: Young, Peter R.
APPLICANT: Zou, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT
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                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US --t
FILING DATE: 04-JUN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A Method of Identifying Agonists and TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3 TITLE OF INVENTION: and TR5 FILE REFERENCE: GH50031
                                                                                                                                                                                                                                                                               COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rauch, Charles
APPLICANT: Walczak, Henning
TITLE OF INVENTION: Receptor That Binds TRAIL
                                       PRIOR APPLICATION DATA:
                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
                                                                                                              APPLICATION NUMBER: US 08/829,536 FILING DATE: 28-MAR-1997
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CITY: Seattle,
                       APPLICATION NUMBER:
                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/883,036A
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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MBER: US 08/799,861
13-FEB-1997
                                                         JMBER: US 08/815,255
12-MAR-1997
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100.0%; Pred. No. 9.8e-06;
Live 0; Mismatches 0;
                                                                                                                                                                                        --to be assigned--
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US-08-931-820-4
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                             Matches
                                                        Query Match
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                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1057 amino aci
                                                                                                                                                                                                                         TOPOLOGY: 111154.
MOLECULE TYPE: pro
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                                                                                                                                                                                                            HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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                                                                                                             OTHER INFORMATION: /label= modified OTHER INFORMATION: /note= "Ala may i
                                                                                                                                                                                 ORGANISM: Homo sapiens
TISSUE TYPE: Collagen type III
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                          Local
                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 76.9 nes 10; Conservative
                                                                                                                                                      NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/931,820
2 SPGTPAPAAEETMTTSPG 19
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                          Similarity 44.4
8; Conservative
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amino acid
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76.9%;
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                                      48.08;
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                       Score 48; DB 3; Le
Pred. No. 1.4e+02;
' wismatches 6;
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Pred. No. 9
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969 APGSPGPAGQQGAIGSPG 986

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RESULT 6
US-09-570-573-21
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                                                                                                                                                                                                                 Patent No. 634200 Patent No. 63420 Patent N
                                                                                                                                                                                                                                                                                                                                 Sequence
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TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICATION NUMBER: US/08,
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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APPLICANT: Bonde, Martin
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carr
TITLE OF INVENTION: Method and Use of the Method to Diagnose the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
APPLICANT: Qvist, Per APPLICANT: Bonde, Martin APPLICANT: Bonde, Martin TITLE OF INVENTION: A Method for Assaying Collagen Fragments TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPHAX: 212-753-6237
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 44.48; hes 8; Conservation
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CLASSIFICATION: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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REGISTRATION NUMBER: 29,714
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40. 6342361
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805 Third Avenue
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Pred. No. 1.4e+02;
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the Presence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
COUNTY: 10022
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
PC-DOS/MS-D
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ORGANISM: DOMCE:
IMMEDIATE SOURCE:
OTONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                          TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence
TITLE OF INVENTION: Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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NAME: GOGORIS, Adda C
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                                                                                                                                                                                       NUMBER OF SEQUENCES:
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APPLICANT: Bonde, Martin
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TELEX: 236687
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CITY: New York
STATE: New Yor
                                                                                                                   CITY: New York
STATE: New York
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REGISTRATION NUMBER:
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805 Third Avenue
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Pred. No. 1.4e+02;
Pred. No. 1.4e+02;
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Best Local
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TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9
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CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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CTTY: Washington
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APPLICANT: TIMM,
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                     APPLICATION NUMBER: FILING DATE: 09-JU
                                                                                                                             SOFTWARE: PatentIn Release #1.0,
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TYPE: amino acid
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REGISTRATION NUMBER:
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FR 94/10585
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Pred. No. 1
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US-08-793-701-41
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US-08-793-701-39
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                         TELEFAX: (202) 408-440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/FR
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                         REGISTRATION NUMBER: 34,872
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ENGTH:
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DUNNER, L.L.P.
                                                                                                                         (202)
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09-JUN-1997
                                                                                      408-4400
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47.48;
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                                                                                                                                                                                                                                                                                                                                     FR 94/10585
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RESULT 10
US-08-793-701-57
; Sequence 57, Ap
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                                                                                                                     ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-793-701-57
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Best Local :
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                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR9501133
PILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: FR 94/10585
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/V
FILING DATE: 09-UUN-1997
CLASSIFICATION: 435
PRIOR ADDITION: 435
                                                                                                                                                                                                                            TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,872
REFERENCE/DOCKET NUMBER: 02356.0075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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nes 9; Conserv
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT ADDRESSEE: DUNNER, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TSPGTPAPAAEETMTTSPG 19
                                             Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                  NAME: McDonell, Leslie A. REGISTRATION NUMBER: 34,8
                                                                                                                                                             STRANDEDNESS:
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1 TSPGTPAPAAEETMTTSPG 19
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                                                                                                                                                                                           284 amino acids
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linear
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SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                         (202) 408-4132
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09-JUN-1997
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47.48;
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                                                           47.08;
47.48;
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                                             Score 47; DB Pred. No. 47; 2; Mismatches
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US-08-415-655-5
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; Patent No. 6025480; GENERAL INFORMATION:
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US-08-415-655-5
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Best Local Similarity
Matches 9; Conserv
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TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                             APPLICANT: Massague, Joan
APPLICANT: Lee, Mong-hong
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: D75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES
TITLE OF INVENTION: SAME
TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 17.
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CORRESPONDENCE ADDRESS:
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                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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                                  ADDRESSEE:
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SEE: Cooper & Dunham: 1185 Avenue of the New York
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1185 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States of America
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50.0%;
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Pred. No. 1e+(
4; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Appli
Patent No. 6025480
              FILING DATE:
CLASSIFICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE,DOCKET NUMBER: 1747
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Massague, Joan APPLICANT: Lee, Mong-hong TITLE OF INVENTION: ISOLATITLE OF INVENTION: 975KIL
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
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LENGTH: 348 amino acids
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OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FILING DATE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 TPPATPAPASD -- LTSDP 167
                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: not
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(212) 278-0400
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                                  1747/47418
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Pred. No.
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31 SGPGQPAPAATQAAPQAP 48

1 TSPGTPAPAAEETMTTSP 18

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        Matches
                                    Query Match
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,516
FILING DATE: 01-DEC-1994
                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: SIGNALLING DOMAIN THERRIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 26
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      Local Similarity
nes 8; Conserv
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TELEX: 133521
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TOT BEAX: 201 343-1684
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TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26.742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELEPONE: 201 487-5800
TELEFAX: 201 343-1684
TINFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: mino acids
TYPE: mino acids
TYPE: protein
US-08-476-509B-4
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Search completed: August 13, 2002, 08:30:32 Job time: 66 sec
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GENERAL INFORMATION:
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Best Local Similarity 44.4
Matches 8; Conservative
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APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEM
APPLICANT: HENRY, CHEM
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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STATE: New Jersey
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411 Hackensack Avenue
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Pred. No. 1.4e+02;
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Maximum DB seq length: 2000000000
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Perfect score:
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TRAIL receptor without intracellular domain; TRID; TNFR-5; human; tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand; haematopoietic tissue; immune system; ligand; apoptosis; treatment.
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                                                                                                                                                                                                                             This sequence represents a human TRID (TRAIL (TNF-related apoptosis-inducing ligand) receptor without an intracellular domain). PRID is a member of the tumour necrosis factor receptor (TNFR) family also known as TNFR-5. TRID is expressed in haematopoietic tissues and other normal human tissues. For a number of immune system-related disorders, substantially altered (whether increased or decreased) levels of TRID gene expression can be detected, therefore the TRID polypeptides, nucleic acids and antibodies are useful in the diagnosis of such immune system related disorders. Mutations of the TRID gene can also be detected. TRID can also be used to identify ligands which may be useful in the treatment of apoptosis related disorders. TRID is administered to humans at a parenteral dose of 0.01 to 1 mg/kg/day.
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tumour necrosis factor receptor family that binds to Apo-2 ligand. Its amino acid sequence was deduced from the nucleotide sequence of an isolated cDNA clone (see AAV84347); an alternative translation initiation site in this clone will encode a polypeptide (see AAW88409); comprising amino acid residues -40 to 269 of Apo-2DcR. Apo-2DcR shows more semmence identity to now in the contraction of the contraction o
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n; autoimmune disease; inflammation;
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Apo-2DcR, or chimeras comprising Apo-2DcR or its (claimed) extracellular domain fused to a heterologous polypeptide are used to modulate apoptosis of mammalian cells (claimed) and/or NF-KappaB activation by Apo-2 ligand, and may be expressed in vivo or ex vivo for gene therapy. They can be used in methods for the modulation and diagnosis of apoptosis e.g. in cases of neurodegeneration.
01-DEC-1999

01-DEC-1999

02-DEC-1999

02-DEC-1999

02-DEC-1999

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20-DEC-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO366
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233; Conserv
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99WO-US28634.
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18-FEB - 2000

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24-FEB - 2000

24-FEB - 2000

01-MAR - 2000

20-MAR - 2000

30-MAR - 2000

31-MAR - 2000

31-MAR - 2000
                                                                                                                                                                                                                                                                  polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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30-MAY-2000;
02-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lated, secretory and transmembrane PRO polypeptide used to detect er PRO polypeptides, link bioactive molecules to cells expressing polypeptides, and detect the presence of mammalian tumours e.g. or breast, prostate, cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides.
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IQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA
                                                          PCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD
                                            pctvcksdqkhkssctmtrdtvcqckegtfrnenspemcrkcsrcpsgevqvsnctswdd
                                                                                                       ttarqeevpqqtvapqqqrhsfkgeecpagshrsehtgacnpctegvdytnasnnepscf
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233; Conser
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2000WO-US08439.
2000WO-US13705.
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2000WO-US03565.
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2000WO-US04914.
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2000WO-US04342.
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Goddard A, God
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deforge L, Desnoyers L, Filva
A, Godowski PJ, Gurney AL, Sh
Tumas D, Watanabe CK, Wood WI,
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                                                                                                                                                                 Score 233; DB 22;
Pred. No. 2.4e-233;
; Mismatches 0;
                                                                                                                                                                  Indels
                                                                                                                                                                                             Length
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                                                                                                                                                                                                259;
                                                                                                                                                                  0;
                                                                                                                                                               Gaps
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                                              146
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RESULT
AAB20111
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                                                                       WPI; 2001-103149/11.
N-PSDB; AAF30053.
                                           diagnosing
                                            New PRO polypeptides, nucleic acids and (ant)agonists, diagnosing and treating immune-related disorders, such
                                                                                                    Wood
                                                                                                            Ashkenazi AJ, Baker KP, Fong
Hillan KJ, Mark MR, Marsters
                                                                                                                                                                             15-MAR-2000; 2000WO-US06884
                                                                                                                                                                                                                 WO200105972-A1
                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO366; UNQ321; human; immune antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20111 standard;
                                                                                                                                                          20-JUL-1999;
                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour necrosis factor receptor; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antirheumatic; antiarthritic; antiinflammatory; antianaemic;
immunosuppressive; antithyroid; antidiabetic; neuroprotective;
hepatotropic; virucide; dermatological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2001
                                                                                                                                        (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunostimulant PRO366 (Apo-2DcR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                          99US-0144758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiallergic; immunostimulant;
                                                                                                                                                                                                                                                              /note= "N
                                                                                                                                                                                                                                            /note=
233..2
                                                                                                                                                                                                                                                                                                                                                                                                       /label=
30..259
                                                                                                                                                                                                                                                                                 /note= "N-myristoylation 114..120
                                                                                                                                                                                                                                                                                                                     56..62
                                                                                                                                                                                                                                                                                                                                                 126..130
                                                                                                                                                                                                                                                                                                                                                                                     /label= Mature_protein 240..257
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                       /note-
                                                                                                                                                                                                                                                                                                            note-
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                                                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune disease; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                         "TNFR/NGFR family cysteine-rich region"
                                                                                                                                                                                                                                                                                                           "N-myristoylation site"
                                                                                                                                                                                                                                  "N-myristoylation site"
                                                                                                                                                                                                                                                    "N-myristoylation
                                                                                                                                                                                                                                                                       "N-myristoylation
                                                                                                                                                                                                                                                                                                                                       "CAMP-
                                                                                                                                                                                                                                                                                                                                                                            "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                               Signal_peptide
                                                                                                                                                                                                                                                                                                                             cAMP- and cGMP-dependent phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
                                                                                                            SA,
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                                                                                                            Goddard A,
Pitti RM,
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                                                                                                                                                                                                                                                                        site'
                                                                                                            Godowski
Tumas D,
                                                                                                                                                                                                                                                                                                                                       protein kinase
                                           , useful for as multiple
                                                                                                            PJ, Gurne
Watanabe
                                            multiple
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                                                                                                                     Gurney AL;
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The present sequence

is

that English

of PRO366 (UNQ321),

also

designated

Claim 20; Fig sclerosis,

8; 127pp;

rheumatoid

arthritis

and

diabetes

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RESULT
AAB36696
ID AAB3
XX
AC AAB3
XX
DT 15-M
XX
DE Huma
XX
KW Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC laimed compositions comprising a PRO polypeptide or its antagonist CC laimed compositions comprising a PRO polypeptide or its antagonist CC have the opposite effect. A claimed method for treating an immune CC related disorder, such as a T cell disorder, involves administering CC a PRO polypeptide, an agonist antibody or an antagonist antibody. CC The disorder is selected from systemic lupus erythematosus, composition, systemic sclerosis, idiopathic inflammatory CC myopathy, Sygren's syndrome, systemic vasculitis, sarcoidosis, CC autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, composition, diabetes mellitus, immune-mediated renal disease, composition, diabetes mellitus, immune-mediated renal disease, composition, composition, inflammatory bowel disease, composition, composition, inflammatory bowel disease, composition, composition, inflammatory bowel disease, composition, inflammatory bowel diseases (such as graft rejection and graft-versus-host disease), inflammatory bowel diseases (such as graft rejection and graft-versus-host disease), inflammatory bowel diseases (such as graft rejection and graft-versus-host disease), call claimed). CC disease of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease), call claimed). CC disease of the proposition of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo-2DcR, a novel human immunomodulator (27 kDa, pI 4.84), as deduced from a human breast carcinoma cDNA clone (see AAF30053).

Apo-2DcR shows homology to apoptosis-linked receptors of the tumour necrosis factor receptor family, such as DR4 and Apo-2. The invention provides polynucleotides (see AAF30050-62) encoding novel human PR0 proteins (see AAB20108-20) including PR0366. Claimed compositions
Human; tumour necrosis TRAIL receptor without
                                                                                           Human tumour necrosis factor receptor 5 (TRID) protein
                                                                                                                                                                   15-MAR-2001
                                                                                                                                                                                                                                                                                                 AAB36696 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQCVEEEGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA
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                                                                                                                                                                (first entry)
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intracellular
                                  factor receptor 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 233; DB 22;
Pred. No. 2.4e-233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
domain; diagnosis;
                              TRID; TNFR-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                               SEQ ID
cytostatic;
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parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; the intermed of the processed apoptotic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activities; and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR 5 or TR5). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding a TRID polypeptide, also referred to as necrosis factor receptor 5, useful in the diagnosis, treatment prevention of cancer, autoimmune disorders and viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive; neuroprotective; antiviral; antiinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Fig 1; 285pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wei Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200071150-A1.
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
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                                                                              disorders; (c) cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0135164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                              diseases associated with disorders; and (e) viral
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Best Local
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                                                   147
                                                                                                                                                                                            Local 5.
233;
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                                                                                                                                                     27
PCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD 120
                                                                                                                                                  ttarqeevpqqtvapqqqrhsfkgeecpagshrsehtgacnpctegvdytnasnnepscf 86
                                                                                                                                                              TTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCF 60
                                                               IQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA
                                                                                                  {\tt pctvcksdqkhkssctmtrdtvcqckegtfrnenspemcrkcsrcpsgevqvsnctswdd}
                                                 iqcveerganatvetpaaeetmntspgtpapaaeetmntspgtpapaaeetmttspgtpa
                                                                                                                                                                                                  h 100.0%;
Similarity 100.0%;
33; Conservative
                                                                                                                                                                                                   0;
                                                                                                                                                                                                  Score 233; DB
Pred. No. 2.4e-
; Mismatches
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                                                                                                                                                                                                   Indels
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RESULT AABSJULT AABSJ
The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein. PRO nucleic acid
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14-MAR-1999
14-MAY-1999
02-JUN-1999
23-JUN-1999
26-JUL-1999
26-JUL-1999
01-SEP-1999
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30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiac hypertrophy; cardiovascular disorder; endotherial unsured angiogenic disorder; atherosclerosis; osteoporosis; hypertension; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; Alzheimer's disease; Huntington's disease; stroke; drug screening
                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid for producing a PRO polypeptide, anal-
genetic disorders and treating cardiovascular, endothelial or
angiogenic disorders, such as atherosclerosis, wounds or cancer
                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ashkenazi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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, Kuo SS, Mark MR,
Williams PM, Wood '
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                                                                                                                                                                                                                                                  FLAG-epitope tag; transmembrane domain; death domain; apoptosis; cell suicide; tissue homeostasis; cell proliferation; cell-cell signalling; Trail Receptor without Intracellular Domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat
                                                                                                                                                                                                                                                                                                                FLAG-TRID
                                         WO200114542-A1
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250..268
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                                                                                                                                                                                          Location/Qualifiers
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                                                                     Transmembrane_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC domain (TM) of a membrane-spanning protein. The method comprises

CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane

CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID)

CC by replacing the nucleic acid encoding the TM of the DD-lacking

CC membrane-spanning protein with a candidate nucleic acid sequence to

CC produce a nucleic acid encoding a modified DD-lacking membrane spanning

CC protein. The modified nucleic acid is then transfected into a host cell,

CC which expresses a DD-containing receptor. The absence of apoptosis of the

CC host cell is determined following exposure of the transfected cell to an

CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent

CC apoptosis of the host cell. The modified nucleic acid encoding the

CC modified death domain-lacking membrane-spanning protein can also include

CC a FLAG-TRID clone, which was used in the method of the present sequence is

CC a FLAG-TRID clone, which was used in the FLAG-epitope tag. The

CC redit suicide DD-lacking membrane-spanning protein and the FLAG-epitope tag. The

CC redit suicide and tissue homeostasis, and to evaluate, interfere and treat

CC events, such as cell proliferation and cell-cell signalling pathways.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a transmembrane domain of a membrane-spanning protein useful in defining processes in cell suicide and tissue homeostasis, comprises modifying the nucleic acid encoding a death domain-lacking
  Human tumour necrosis related receptor TR5
                                          11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                              AAW76331;
                                                                                                                     AAW76331 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                         PCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD
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)B; AAH19325.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                      (first entry)
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CC invention provides methods for the recombinant production of TR5 CC and its use in diagnostic and therapeutic methods. Treatment of a subject in need of enhanced TR5 activity comprises administering an CC agonist to the polypeptide and/or providing TR5 polynucleotide in a CC form so as to effect production of the polypeptide activity in vivo. CC Treatment of a subject with the need to inhibit TR5 polypeptide activity comprises administering an antagonist to the polypeptide activity comprises administering an antagonist to the polypeptide, concleotide sequence encoding the polypeptide for its ligand, substrate or receptor. Diagnosing a disease or a susceptibility comprises determining the presence or absence of mutation in the concleotide sequence encoding the Presence of mutation in the concleotide sequence encoding the presence or absence of mouleotide sequence encoding the TR5 polypeptide in the genome of the subject and/or analysing for the presence or amount of TR5 comprises determining the ample. Identification of compounds CC which bind to TR5 comprises contacting host cells with a candidate compound and assessing the ability of it to bind to the cells. The californic and acute in flammation. arithritis, senticemia, autoimmune diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis related receptor; TR5; human; inflammation; arthritis; septicaemia; transplant rejection; autoimmune disease; inflammatory bowel disease; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; psoriasis; restenosis; brain injury; AIDS; bone disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury, AIDS and bone diseases
        graft vs host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atherosclerosis and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone (see AAV56990).
protein that has a mem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of human tumour necrosis related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 1;
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05-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lyn SDP,
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                                                                                                                                                            inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor TR5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tan KB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as deduced
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97US-0795910.
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1..165
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e.g. lymphops
d Alzheimer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane proximal O-glycosylation region
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The protein is characterised as a GPI-1
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       AAZ21103 to AAZ21102 encode new human secreted proteins and AAZ29861 to AAZ29873 represent the secreted proteins encoded by the polynucleotide sequences. AAZ21103 to AAZ21112 represent probes for the secreted proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic and thrombolvtic activity, reconstruction cannot be activity.
                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1998;
14-MAY-1998;
10-MAR-1999;
                                                                                                                                                                               Claim 17; Page 104; 118pp; English.
                                                                                                                                                                                                            Polynucleotides encoding secreted human fetal brain, human adult blood, human ac neural tissue cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9946287-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; biological activity; nutritional; cytokine; cell proliferation; differentiation; immune stimulating; vaccine; haematopolesis regulation; tissue growth; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted
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                                                                                                                                                                                                                                                                                                      7 K,
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Treacy M,
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98US-0079124.
99US-0266105.
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Agostino MJ,
 receptor/ligand
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; Mismatches 0;
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Steininger RJ;
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adult bladder,
activity,
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Best Local Similarity
Matches 233; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides and proteins can also be used as nutritional sources or supplements. Such uses include use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. They may also have utility in compositions used for bone, cartilage, tendon, ligament, and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers. The proteins which induce cartilage and/or bone growth in circumstances where bone is not normally formed, have application in the healing of bone fractures and cartilage damage or defects in humans and other animals.
                                                                                                                                                                                                                                                                                                Tumour necrosis factor receptor; TR5; TRID; DcR1; agonist; antagonist; screening; human; cancer; AIDS; Alzheimer's disease; inflammation; arthritis; septicaemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; restenosis; brain injury;
                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                      bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY05744;
Identifying agonists and antagonists of tumor necrosis related receptors TR1, TR3 and TR5, and of ligand TL3,
                                                                                                                                                                 02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                              WPI; 1999-246560/21
                                                                                                                                      08-OCT-1997;
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                                                                                                                                                                                                                            EP911633-A1
                                                                                                                                                                                                                                                                                                                                                                                                        Tumour necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY05744 standard;
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                                                                                                                                                                                                                                                                                      disease;
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                                                                                                       SMITHKLINE BEECHAM CORP
                                                                           PC,
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                                                                                                                                                                                                                                                                                     atherosclerosis; therapy
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                                                                                                                                      97US-0061334
                                                                                                                                                                   98EP-0203332
                                                                                                                                                                                                                                                                                                                                                                                                       factor receptor
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Pred. No. 2.8e-233;
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useful
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compounds that bind to the receptors or ligand, and which activate
(agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or
TL3. A screening kit for identifying agonists, antagonists,
ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or
TL3 polypeptides is provided. The agonists and antagonists are
useful for treatment of chronic and acute inflammation, arthritis,
septicaemia, autoimmune disease e.g. inflammatory bowel disease,
psoriasis, transplant rejection, graft versus host disease,
infection, stroke, ischaemia, acute respiratory disease syndrome,
restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
lymphoproliferative disorders), atherosclerosis and Alzheimer's
disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.
                                                                                                                                                                                          autoimmune disease; viral infection; degenerative disorder; amyotrophic lateral sclerosis; retinitis pigmentosa; ischae cerebellar degeneration; myelodysplastic syndrome.
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                                                                                                                                                                                                                                                                   Human TRAIL-R3 protein sequence.
                                                                                                                                                                                                                                                                                                                                                            AAY00933 standard; Protein;
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               (IDUN-) IDUN
                                           15-AUG-1997;
                                                                       14-AUG-1998;
                                                                                                     25-FEB-1999
                                                                                                                                   WO9909165-A1
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es 233; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFR) TR5, also known as TRID or DcR1. The invention relates TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and eir ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                 IQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA 180
                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD 120
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                                                                                                                                                                                                                                       DR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents tumour necrosis factor receptor also known as TRID or DcRl. The invention relates
                                                                                                                                                                                                                                       DR5s; TRAIL-R3; apoptosis related condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer, AIDS, Alzheimer's disease, bone disease
               PHARM INC
                                           97US-0055906
                                                                       98WO-US16945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23pp; English.
                                                                                                                                                                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 233; DB 20;
Pred. No. 2.8e-233;
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                                                                                                                                                                                                           ischaemic
                                                                                                                                                                                                                                     cancer; therapy;
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This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An antibody against the TRAIL receptors is useful for detecting mammalian DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins. (Ant)agonists identified by the assay are useful for modulating the apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Proteins activity mediated by DR5 or TRAIL-R3 proteins Apoptosis related conditions which are treated in this way, include cancer (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus are treated in the proteins and immune-modiated define the proteins and immune-modiated states.
                                                 sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial infarction and stroke). The polynucleotides can alone be used to treat these diseases. Antisense oligonucleotides to the DNA sequences can be used to form a composition that is useful for inhibiting expression of a human DR5 or TRAIL-R3 protein.
                                                                                                                                                                                                                     erythematosus and immune-mediated glomerulonephritis), viral infections (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 62-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newly isolated polynucleotide encoding a mammalian TRAIL receptor protein - useful in for screening for (ant)agonists that modulate the apoptotic activity mediated by DR5 or TRAIL-R3 proteins
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Sequence
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Matches
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                                                                                                                                        PCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD 120
                                                                             IQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA 180
                                                                                                                                                                                   ttarqeevpqqtvapqqqrhsfkgeecpagshrsehtgacnpctegvdytnasnnepscf 126
                                                                                                                        \verb|pctvcksdqkhkssctmtrdtvcqckegtfrnenspemcrkcsrcpsgevqvsnctswdd|
                                                             iqcveefganatvetpaaeetmntspgtpapaaeetmntspgtpapaaeetmttspgtpa
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                               Score 233; DB 20;
Pred. No. 2.8e-233;
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Length

299;

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AAW94671 standard;
                      12
Protein;
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밁 Š 뫄 QΥ Ъ Qy В Q

Human TNF-related apoptosis-inducing ligand binding protein

04-MAY-1999

(first entry)

Human; TNF-related apoptosis-inducing ligand binding protein; clotting; TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy; thrombotic microangiopathy; thrombotic thrombocytopenic purpura; haemolytic-uraemic syndrome; systemic lupus erythematosus.

Homo sapiens

AAW94671
IID AAW
XX
AC AAW
XX
AC AAW
XX
DT 04-1
DT 04-1
DT TAA
XX
HUMB
XX
HUMB WO9900423-A1

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RESULT 1
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ID AAW88409
AC AAW8

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Best Local
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                                                                                                                                                                                 therapy.
                                                                                                                                                                                                                                                                                        Human Apo-2DcR
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW88409 standard; Protein;
                                                   Peptide
                                                                                                                                 Homo sapiens
                                                                                                                                                                                                            neurodegeneration;
                                                                                                                                                                                                                                    Apo-2DcR; human;
                                                                                                                                                                                                                                                                                                                                           26-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated TRAIL binding protein - which binds to a tumour rosis factor-related apoptosis inducing ligand, used in tignosis and treatment of TRAIL-mediated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCF 60
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/note=
41..69
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                  apoptosis; tumour necrosis factor receptor;
                                                                                                                                                                                                            autoimmune
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                     "-40 to -1 region of Apo-2DcR"
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Pred. No. 2.8e-233;
                                                                                                                                                                                                          disease; inflammation; cancer;
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not express
                                                                                                                     This polypeptide comprises human Apo-2DcR, a novel member of the
                                                                                                                                                   New Apo-2DcR polypeptide - used for modulation and diagnosis of
                                                                                                                                                                                        Ashkenazi AJ,
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DB; AAV84347.
                                                                                                                                  9; Page 53-54;
                                                                                                                                                                                  Wood
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Apo-2DcR transcripts,
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                                                                                                                                              neurodegeneration
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                                                                                                                                                                                                                                                                                                           "N-glycosylation"
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                  A pure or recombinant polypeptide which binds to a polyclonal antibody specific for the mature UL144 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known, which include the CD95 [Fas/APO-1], the TNF receptor-1, TNF receptor apoptosis-mediated approach to the condition of the condition of the condition of viral infection and replication. At least five different death receptors are known, which include the CD95 [Fas/APO-1], the TNF receptor-1, TNF receptor apoptosis-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leong
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hes 233;
                                                                                                                                                                                                                                                                                                                                                                 sequence which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                death receptor; apoptosis; programmed cell death; FAS;
; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; vi
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                                                                                                                                                                                                                                                                                   Page 75-76; 76pp;
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Pred. No. 2.8e-233;
                                                                                                                                                                                                                                                                                   English.
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6 (DR-6), and TNF-related
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Best Local S
Matches 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLAG-epitope tag; transmembrane domain; death domain; apoptosis; cell suicide; tissue homeostasis; cell proliferation; cell-cell signalling; Trail Receptor without Intracellular Domain;
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                                                              Identifying a transmembrane domain of a membrane-spanning protein useful in defining processes in cell suicide and tissue homeostasis, comprises modifying the nucleic acid encoding a death domain-lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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Pred. No. 2.8
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No. 2.8e-233;
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CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane
CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID)
CC by replacing the nucleic acid encoding the TM of the DD-lacking
CC membrane-spanning protein with a candidate nucleic acid sequence to
CC produce a nucleic acid encoding a medified DD-lacking membrane spanning
CC which expresses a DD-containing receptor. The absence of apoptosis of the
CC host cell is determined following exposure of the transfected cell to an
CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent
CC apoptosis of the host cell. The modified nucleic acid encoding the
CC modified death domain-lacking membrane-spanning protein can also include
CC a nucleic acid sequence encoding an epitope tag. The present sequence is
CC affac-epitope is a useful marker to purify proteins encoded by the
CC modified DD-lacking membrane-spanning protein. The present invention.
CC TAG-epitope is a useful marker to purify proteins encoded by the
CC modified DD-lacking membrane-spanning proteins and the first end treat
CC membrane-spanning proteins may be used in defining processes involved in
CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat
CC events, such as cell proliferation and cell-cell signalling pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
                                   05-SEP-1997;
                                                                                               04-SEP-1998;
                                                                                                                                                              11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                       cytoplasmic domain;
                                                                                                                                                                                                                                 W09911791-A2
                                                                                                                                                                                                                                                                                                                                                                       apoptosis; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human hAPO9 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paaeetmttspgtpapaaeetmttspgtpasshy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCTVCKSDQKHKSSCTWTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iqcveefganatvetpaaeetmntspgtpapaaeetmntspgtpapaaeetmttspgtpa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                               98WO-US18393
                                                                                                                                                                                                                                                                                                                                                                                                   1mmunogen;
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                                                                                                                                                                                                                                                                                                                                                                                                       antibody
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                                                                                                                                                                                                 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TWF related ligands 1 and 3 (TNRL1 and TNRL3) or CC fragments, and isolated TWF related ligands 1 and 3 (TNRL1 and TNRL3) or CC their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic CC molety. APO4 polypeptides are also useful for identifying selective comolety. APO4 polypeptides are also useful for identifying selective cancer can also useful to the polypeptides are the polypeptides are also useful for comparison or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC for agonists and antagonists by binding and observing the changer in APO4 cativity. Effective pharmacological agents useful in diagnosis or CC treatment of disease are also identified using APO4 polypeptides/active fragments are also seful in diagnosis or CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4 cativity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also CC useful for diagnosis/treatment of developmental or gestational cc abnormalities. APO8 was transfected to human breast carcinoma cell line of CC and an although a change a change of the compared to the
                                                            Matches
                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental or gestational abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-205191/17
N-PSDB; AAX23412.
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                     MCF-7, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNIW ) UNIV WASHINGTON.
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                                                                                   Local
                                                            185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Fig 6; 156pp; English
                                                                                   Similarity
                                                                                                                                                                                                 259
                                                                                                                                                                                                                                                        induced apoptosis.
                                                         Conservative
                                                                                79.4%;
                                                         0,
                                                                             Score 185; DB 20;
Pred. No. 1.5e-183;
                                                         Mismatches
                                                         0;
                                                                                                          Length 259;
                                                         Indels
                                                         0
                                                      Gaps
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207
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                                   PAAEE 185
                                                                                          IQCVEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPA
                                                                                                                                                                      PCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD 120
paaee
                                                                                                                                                                                                                           ttarqeevpqqtvapqqqrhsfkgeecpagshrsehtgacnpctegvdytnasnnepscf
                                                                        iqcveefganatvetpaaeetmntspgtpapaaeetmntspgtpapaaeetmttspgtpa
                                                                                                                                                     pctvcksdqkhkssctmtrdtvcqckegtfrnenspemcrkcsrcpsgevqvsnctswdd
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                 Mammalia
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                                                                                                                                                                    therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                       necrosis
                                                                                                                                                                                                                                                  tumour necrosis factor receptor; apoptosis; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                              factor receptor
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Best Local
                                                                                                                                                                                                            for preventing or reducing the advancement, severity or effects of an immunological disease involves administering a TRAIL-R2 or TRAIL-R3 blocking agent such as a soluble TRAIL-R (preferably comprising a human immunoglobulin Fc domain) and an antibody. A method of treating cancer involves administration of antibodies against TRAIL-R3 or TRAIL-R2. A method of inducing cell death involves administration of an agent capable of inhibiting the
                                                                                                                                                                                                                                                                                                    a putative glycosylphosphatidylinositol-anchored protein, which is either cell-associated or processed and secreted. Secreted TRAIL-R3 competes for the binding of TRAIL to TRAIL-R1 and/or TRAIL-R2, thereby acting as an inhibitor of apoptosis. Expression of TRAIL-R3 is restricted to peripheral blood lymphocytes and skeletal muscle. It is likely that TRAIL-3 acts as an important regulator of TRAIL-R2 and -R3 induced cell death in vivo. A method
                                                                                                                                                                                                                                                                                                                                                                                             cysteine-rich receptor of the tumour necrosis factor receptor. The invention is related to novel receptors for TRAIL, i.e. 7 (see AAY05725) and TRAIL-3. TRAIL-3 is highly glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents TRAIL-R3, a novel mammalian constant receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1998;
12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                involves administration of an binding of TRAIL-R2 or -R3 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tschopp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel tumor necrosis factor receptor proteins TRAIL-R2 and TRAIL-R3
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     180
                                                       120
                             154
                                                                                                        Local Similarity 100.
hes 140; Conservative
                                                                                 94
                                                                  NSPEMCRKCSRCPSGEVQVSNCTSWDDIQCVEEFGANATVETPAAEETMNTSPGTPAPAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-276942/23
eetmntspgtpapaaeetmttspgtpapaaeetmttspgtpapaaeetmttspgtpassh
                            EETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSH
                                                     nspemcrkcsrcpsgevqvsnctswddiqcveefganatvetpaaeetmntspgtpapaa
              259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 28;
                                                                                                                                                                          AA;
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97US-0058631.
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238..259
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176..1
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.e= "TAPE repeat"
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                                                                                                                     60.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "transmembrane domain"
                                                                                                          0;
                                                                                                                     Score 140; DB 20;
Pred. No. 6.8e-137;
                                                                                                                                                                                                its ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide"
                                                                                                          Mismatches
                                                                                                          0;
                                                                                                                                 Length 259;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                        A method
                                                                                                        0;
                                                                                                       Gaps
                           213
                                                     179
  239
                                                                                                        0
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AAW98200
ID AAW9
XX
AC AAW9
XX
DT 05-J
XX

AAW98200

standard;

Protein;

386

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19

AAW98200; 05-JUL-1999

(first entry)

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RESULT :
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 В
                      δÃ
                                                                                                        Query Match
Best Local
                                              Matches
                                                                                                                            This peptide is encoded by DNA21705, a cDNA clone obtained by PCR amplification (see AAV84349-50) of human breast carcinoma cDNA. The peptide shows homology to a peptide (see AAW88449) derived from human tumour necrosis factor receptor 1 (TNFR1). DNA21705 was used as a probe to screen a human foetal lung library, yielding a clone (see AAV84347) encoding Apo-2DcR, a novel member of the TNFR family that binds to Apo-2 ligand and is involved in apoptosis. Apo-2DcR polypeptides can be used in methods for the modulation and diagnosis of apoptosis e.g. in cases of neurodegeneration, autoimmune diseases and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9858062-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Apo-2DcR peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW88450 standard;
                                                                                                                                                                                                                                                                                   New Apo-2DcR
apoptosis, e.
                                                                                                                                                                                                                                                                                                                                              ETX
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW88450;
                                                                                                       Sequence
                                                                                                                                                                                                                                                             Example 1; Page 39; 88pp; English.
                                                                                                                                                                                                                                                                                                                       WPI; 1999-095340/08
                                                                                                                                                                                                                                                                                                                                                         Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apo-2DcR; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 CNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKE 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
 _
cnpctegvdytnasnnepscfpctvcksdqkhkssctmtrdtvcqcke
                                              . Similarity 48; Conserv
                                                                                                                                                                                                                                                                                                                                              Wood
                                                                                                        48
                                              Conservative
                                                                                                                                                                                                                                                                                   polypeptide -
.g. in neurodec
                                                                                                                                                                                                                                                                                                                                              WI;
                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                        Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                       97US-0878168
                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US12456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apoptosis; tumour necrosis factor receptor;
n; autoimmune disease; inflammation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide;
                                                                                                                                                                                                                                                                                    neurodegeneration
                                                        20.6%; Score 48; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233
                                                                                                                                                                                                                                                                                                                                                        Chuntharapai A,
                                                                                                                                                                                                                                                                                               used for modulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                              Mismatches
                                             DB 20; I
3.6e-42;
hes 0;
                                                                                                                                                                                                                                                                                                                                                        Gurney
                                                                                                                                                                                                                                                                                                 and
                                                                   Length 48
                                                                                                                                                                                                                                                                                                 diagnosis
                                             0;
                                                                                                                                                                                                                                                                                                 of
                                              Gaps
                                              0
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RTD,

inhibitor of

Apo-2 ligand-induced apoptosis

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The present sequence is human RTD, a novel protein capable of binding Apo-2 ligand. RTD is a receptor for tumour necrosis factor, belonging to the family of trail receptors. It is an initial content of the family of trail receptors. It is an economic factor, belonging to the family of trail receptors. It is an economic factor, belonging to the family of trail receptors. It is an economic factor for the sequence and the factor factor factor factor for the vectors deposited as ATCC 209201 cencoded by the cDNA insert of the vectors deposited as ATCC 209201 or ATCC 209202 (see also AAX25093). These cDNAs differ in sequence at a single nucleotide, resulting in serine or leucine at amino acid position 310 of RTD. Isolated RTD polypeptides, especially the extracellular domain (ECD), chimeric molecules including RTD or its ECD, and nucleic acids encoding such polypeptides are claimed, as are antibodies, vectors, host cells (especially CHO, yeast and
                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                 Claim 4; Page 40-52; 58pp; English
                                                                                                                                                                                                                                                                                                                                       A new polypeptide, designated
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9910484-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis
                                                                                                                                                                                                                                                                                                                                                                                1999-254218/21
)B; AAX25093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0918874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US14552
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310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N-glycosylated"
171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213..232
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99..139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
56..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41..180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor receptor; trail receptor; Apo-2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                           Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "extracellular domain specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "extracellular domain specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "extracellular domain,
in Claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "extracellular domain specifically claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ser, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in Claim
                                                                                                                                                                                                                                                                                                                                           RTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide
in Claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide,
in Claim 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide
in Claim 8"
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Query Match Best Local

Similarity

6.0%;

Score 14; Pred. No.

DB 20; 4.5e-06;

Length 386

Sequence

386

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RESULT
AAY04144
QY
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Best Local :
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                                   The present sequence represents human Tango-74. Tango polypeptides are useful for identifying compounds which bind the polypeptide via direct binding, competition binding assays or Tango-71, -73, -74, 76 or -83 mediated signal transduction. Tango polypeptides are also useful for identifying modulating compounds by determining effect on Tango activity Tango polypeptides and nucleic acids are useful for diagnosing diseases related to aberrant expression of Tango, and Tango polypeptides are useful for raising antibodies which can be used in diagnostic assays for detection of Tango, and also for generating anti-idiotype antibodies for
                                                                                                                                                                                                      New TANGO polypeptides diagnostic agents and f expression of TANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E coll cells), transgenic and knockout animals, and a method of modulating apoptosis in mammalian cells by exposing the cells to RTD polypeptide. This therapy can be accomplished e.g. using in vivo or ex vivo gene therapy techniques. RTD chimeric molecules comprising immunoglobulin sequences can be used to inhibit Apo-2 ligand activities, e.g. apoptosis or NT-Kappa B induction or the activity of another ligand to which RTD binds.
                        prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Tango-71; detection.
                                                                                                                                                                             Claim 8; Fig 3; 84pp;
                                                                                                                                                                                                                                                               WPI; 1999-167426/14
N-PSDB; AAX19957.
                                                                                                                                                                                                                                                                                                       Goodearl ADJ,
                                                                                                                                                                                                                                                                                                                                                           05-SEP-1997;
06-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09907850-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Tango-74 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY04144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY04144 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                (MILL-)
                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 tgacnpctegvdyt 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 TGACNPCTEGVDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                 MILLENNIUM BIOTHERAPEUTICS
                        and protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                       Holtzman
                                                                                                                                                                                                                                                                                                                                                           97US-0058108
97US-0054966
                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US16502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%;
                                                                                                                                                                             English
                                                                                                                                                                                                                    and nucleic for treating
                                                                                                                                                                                                                                                                                                       DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 AA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                     acids encoding them . disorders caused by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
4.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                        aberrant
                                                                                                                                                                                                                                    useful
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RESULT 2
AAW99018
JD AAW99018
AAW POT 12-N
AX AAW9
AX AAW9
AX AAW9
AX HUMB
KW HIV
KW TNF
KW MIV
KW TNF
KW MU15
AX HOME
AX AW9
AX TNF
KW MU15
AX TNF
KW MU15
AX TNF
KW MU15
AX TNF
CO TNE
  RESULT 2
AAW99019
ID AAW9
XX
AC AAW9
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                                                                                                                                                                                                                                                     δÃ
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                                                                                                                                                                                                                                                                                                                                                    Query
Best I
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biological activity of TRAIL. TRAILR proteins can be used for treating thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura (TTP) or haemolytic-uraemic syndrome (HUS), clotting of small blood vessels in e.g. AIDS, multiple sclerosis or systemic lupus erythematosus or for reducing TRAIL-mediated death of T cells in HIV-infected patients They can also be used to purify TRAIL or TRAIL-expressing cells or as carriers for delivering agents to cells bearing TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; TRAIL; TRAIL receptor; immunoreactive; thrombotic microangiopathy; HIV infection; tumour necrosis factor related apoptosis inducing ligand; TNF related apoptosis inducing ligand; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated TRAIL receptor polypeptides - used to develop products for treating e.g. thrombotic microangiopathy, multiple sclerosis, systemic lupus erythematosus or HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis-inducing ligand (TRAIL) receptor designated TRAILR4A. TRAILR proteins can be used for binding TRAIL, e.g. to measure or inhibit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 51pp; English.
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                                                           AAW99019 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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DB; AAX18926.
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                                                                                                                                                                                                                                                                                                                                                 Score 14;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour necrosis factor
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. 4.5e-06;
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Query Match
Best Local S
Matches 14
TR10; tumour necrosis factor receptor; TNF; human; agonist; treatment; disease; apoptosis; inhibition; cancer; lymphoma; carcinoma; tumour; autoimmune disease; viral infection; allammation; graft rejection; AIDS; graft versus host disease; antagonist; neurodegenerative disorder; myelodysplastic syndrome; ischemic injury; liver disease; drug screening; septic shock; cachexia; anorexia; detection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis-inducing ligand (TRAIL) receptor designated TRAILR4B. TRAILR proteins can be used for binding TRAIL, e.g. to measure or inhibit the biological activity of TRAIL. TRAILR proteins can be used for treating thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura (TTP) or haemolytic-uraemic syndrome (HUS), clotting of small blood vessels in e.g. ALDS, multiple sclerosis or systemic lupus erythematosus or for reducing TRAIL-mediated death of T cells in HIV-infected patients. They can also be used to purify TRAIL or TRAIL-expressing cells or as carriers for delivering agents to cells bearing TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated TRAIL receptor polypeptides - us
for treating e.g. thrombotic microangiopathy,
systemic lupus erythematosus or HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF related apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9903992-A1
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                                                                                                                                                                   Human
                                                                                                                                                                                                               12-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX
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                                                                                                                                                                TNF receptor TR10 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51pp;
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                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                              106
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                                                                                                                                                                                                                                                                                                           386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour necrosis factor (TNF)-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2v,
3. 4.5e-06;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to develop products hy, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Homo

sapiens.

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CC receptor, TRIO. TRIO polyperbides or agonists can be used for treating CC diseases and disorders associated with inhibition of apoptosis, e.g. CC cancers (e.g. follicular lymphomas, carcinomas with p53 mutations, and CC hormone-dependent tumours, such as breast cancer, prostate cancer, CC (Exposi's sarcoma and ovarian cancer), autoimmune disorders (e.g. systemic CC lupus erythematosus and immune-related glomerulonephritis rheumatoid CC arthritis), viral infections (e.g. herpes viruses, pox viruses and CC adenoviruses), inflammation, graft versus host disease, acute graft CC rejection and chronic graft rejection. Antagonists can be used for treating disease, amyotrophic lateral sclerosis, e.g. AIDS, neurodegenerative disorders (e.g. Alzhelmer disease, CC e.g. AIDS, neurodegenerative disorders (e.g. Alzhelmer disease, CC earmila), ischemic injury (e.g. as caused by myocardial infarction, stroke and reperfusion injury), toxin-induced liver disease (e.g. as caused by calcohol), septic shock, cachexia and anorexia. Antagonists can also be used for treating inflammatory diseases and disorders, e.g. inflammatory cancers and disorders, e.g. inflammatory cancers and disorders, e.g. inflammatory cancers and so be used for treating inflammatory diseases and disorders, e.g. inflammatory cancers and also be used for treating inflammatory cancers and content this, psoriasis and cancers 
RESULT 24
AAB01341
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                                                                                                                                                             Matches
                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human tumour necrosis factor-like receptor TR10 to develop products for treating, e.g. cancers, autoimmune disorders, viral infections, inflammation, graft rejection,
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a novel human tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Fig 1A-D; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1997;
30-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                93
                                                                                                                       37
                                                                                                    TGACNPCTEGVDYT
                                                                                                                                                                                                                                                                                                            screening.
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DB; AAV72101.
                                                                              tgacnpctegvdyt
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                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                 386 AA;
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0069112.
97US-0050936.
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213..230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders
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                                                                                                                                                                                Score 14;
Pred. No.
                                                                                                                                                             Mismatches
                                                                                                                                                                              DB 20;
4.5e-06;
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KKKK KKK DX A X I D

Human 31-MAY-2000 AAY69991;

receptor-associated

protein from Incyte clone 3472455

(first entry)

Human receptor-associated protein; HRAP; Incyte clone 3472455; cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic; antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;

neuroprotective;

treatment;

prevention;

reproductive

disorder;

antiallergic; antidiabetic; dermatological;

antiasthmatic; osteopathic;

AAY69991

25

AAY69991 standard; Protein;

386

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                                                     Query Match
Best Local S
Matches 14
                                                                                                                                      development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known, which include the CD95 (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated protein (TRAMP), death receptor-6 (DR-6), and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.
                                                                                                                                                                                                                                       A pure or recombinant polypeptide which binds to a polyclonal antibody specific for the mature UL144 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or device the polypeptide is also useful to modulating apoptosis.
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 73-74; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Purified or recombinant polypeptide for modulating apoptosis comprises a sequence which binds to an antibody specific for UL144 or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF-related apopotosis inducing ligand
                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-423383/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200034335-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ULl44; death receptor; apoptosis;
TNF-R1; TRAMP; DR-6; TRAIL; modula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB01341 standard; Protein; 386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SCHE ) SCHERING CORP
93
                            37 TGACNPCTEGVDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                c,
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Phillips JH;
                                                                                                                             386 AA;
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0205018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US26035
                          50
106
                                                                   6.0%; Score 14; DB 21; 100.0%; Pred. No. 4.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modulation; treatment; cancer
                                                        0
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TRAIL) receptor-3
                                                                                  Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAS;
                                                     0;
                                                     Gaps
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cardiovascular;

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Key
                            Hillman JL, Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal;
                                                                   07-AUG-1998;
01-SEP-1998;
                                                                                           06-AUG-1999;
                                                                                                                          WO200008155-A2
                                                                                                                                                                       Binding-site
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       N-PSDB;
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                                                    (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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              2000-205710/18
       AAZ50893
                                                    INCYTE
                            Baughn
                                     Yue H,
                                                    PHARM INC
                                                                   98US-0160065
98US-0098703
                                                                                           99WO-US17777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell proliferative; autoimmune; inflammatory; allergy;
1; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
mia; asthma; dermatitis; diabetes; osteoporosis;
sis; irritable bowel syndrome.
                                                                                                                                                                                                                                     /note=
369
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361
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352
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345
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310
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281
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263
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87
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127
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231
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189
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173
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157
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133
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77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                        /label= ATP/GTP_binding_site
99..180
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                             MR;
                                     Lal
                                                                                                                                       "TNFR/NGFR cysteine-rich region"
                                                                                                                                                                             "Potential N-glycosylation
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                                     ۵,
                                    Tang
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                                     YT,
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                                     Gorgone
                                    GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      site"
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                                                                                                                                                                                                                                                                                                                           site"
                                    Guegler
                                    3
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antiarthritic, antirheumatic, osteopathic, antiallergic, antianaemic, antiarthritic, antirheumatic, osteopathic, antiallergic, antianaemic, antiatsthmatic, antidiabetic, dermatological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia,
                                                                                                                                                                                                                                                               and urologic tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic.
                                                                                                                                                                                                                                                                                   and urologic tissues. HRAP
                                                                                                                                                                                                                                                                                                                  This sequence is expressed in musculoskeletal, cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 78-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human receptor-associated proteins (HRAP) useful for the dia
treatment and prevention of cell proliferative, autoimmune,
inflammatory, reproductive, cardiovascular, and gastrointestinal
disorders
Sequence
                                                                    cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and
                                             irritable
                                                                                                                                                                                                                                                                                                                                              (HRAP)
                                                                                                                                                                                                                                                                                                                                                                  present
                                                                                                                                                                                                                                                                                                                                              from
                                           bowel syndrome).
386
                                                                                                                                                                                                                                                                                                                                      sequence is a human receptor-associated protein Incyte clone 3472455 obtained from LUNGNOT27 cDNA
AA;
                                                                                                                                                                                                                                                                                                                                                                                                             99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis,
                                                                                                                                                                                                                                                                                                                                         library.
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δÃ
                      밁
                                                   Matches
                                                                 Query Match
                      93
                             37 TGACNPCTEGVDYT
                                                           Local
26
                     tgacnpctegvdyt 106
                                                   14;
                                                          Similarity
                                                   Conservative
                                    50
                                                          6.0%;
100.0%;
                                                   0;
                                                          Score 14;
Pred. No.
                                                   Mismatches
                                                          DB 21;
. 4.5e-06;
                                                                Length 386;
                                                   Indels
                                                   0;
                                                   Gaps
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0

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breast; pr
cartilage;
  Homo
                                         Human secretory and transmembrane; PRO; mammalian; cancer: breast; prostate; cervical; tumour necrosis factor-alpha; T cartilage; ear; proliferation; glucose; free fatty acid; sk adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                  Human PRO288
                                                                                                                                                                                                                 24-OCT-2001
                                                                                                                                                                                                                                                                AAU12341;
                                                                                                                                                                                                                                                                                                          AAU12341 standard;
sapiens
                                                                                                                                                                polypeptide sequence
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                          Protein; 386
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; lung; ; TNF-alpha; `~letal muscle; skeletal

20-DEC-1999 20-DEC-1999 30-DEC-1999 30-DEC-1999 06-JAN-2000 11-FEB-2000 11-FEB-2000 18-FEB-2000 22-FEB-2000 01-DEC-09-DEC-1999; 16-DEC-1999; 02-DEC-1999 02-DEC-1999 02-DEC-1999 01-DEC-2000; 07-JUN-2001. WO200140466-A2 -1999; -1999; 99US-0170262 99WO-US30095 99WO-US30991 99WO-US30999 99WO-US31243 2000WO-US00277 2000WO-US00376 2000WO-US03565 2000WO-US04341 2000WO-US32678 99WO-US28565. 99WO-US28564 99WO-US28551 99WO-US28634

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AAB31187
ID AAB3
XX
AC AAB3
XC AAB3
XX
DT 20-#
XX
DT 40-#
XX
XX
DE Amir
XX
KW Huma
                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (Thr-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or monocytes, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
20-MAR-2000;
31-MAR-2000;
17-MAY-2000;
17-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
           Human; secreted PRO185; PRO210;
                                                                                                                                                                               AAB31187 standard; Protein; 386 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO
PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000;
02-JUN-2000;
                                                               Amino acid sequence of human polypeptide PRO288.
                                                                                                        20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU12172-AAU12446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gerritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-2000;
                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                            polypeptides. The PRO polypeptides are useful to detect other polypeptides, to link bloactive molecules to cells expressing polypeptides, to modulate biological activities of cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides, and to detect the presence of mammalian lung, ust, prostate, rectal, cervical or liver tumours by comparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-408281/43.
DB; AAS21413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast, prostate,
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENENTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 340; 813pp; English.
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ME, Goddard
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     386
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2000WO-US05004
2000WO-US05601
2000WO-US07377
2000WO-US07377
2000WO-US08439
2000WO-US14042
2000WO-US14042
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US14941.
2000WO-US15264.
         protein;
PRO215; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The PRO polypeptides are useful to detect other
                                                                                                                                                                                                                                                                                                                                                 6.0%; >--
100.0%; Pr
.-- 0;
                                                                                                                                                                                                                                                                                106
                                                                                                                                                                                                                                                                                                                 50
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A, Godowski PJ, Gurney J
Tumas D, Watanabe CK, W
         pRO217; PRO242; PRO288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical or liver tumours by comparing PRO a cell sample to that in a control sample.
                                                                                                                                                                                                                                                                                                                                                       Score 14; DB; Pred. No. 4.5
                                                                                                                                                                                                                                                                                                                                               DB 22,
3. 4.5e-06;
0;
         PRO196;
PRO365;
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                                                                                                                                                                                                                                                                                                                                                                                          Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Filvaroff E,
       PRO444; PRO183;
PRO1361; PRO1308;
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colon,
                                                                                                                                                                                                                                                                                                                                                       0,
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         15-JUN-1999
20-JUL-1999
26-JUL-1999
17-AUG-1999
01-SEP-1999
08-SEP-1999
15-SEP-1999
15-SEP-1999
01-DEC-1999
01-DEC-1999
                                                                                                                                                         22-FEB-2000;
01-MAR-2000;
02-MAR-2000;
20-MAR-2000;
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05-JAN-2000;
18-FEB-2000;
Ashkenazi AJ, Baker
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PRO1600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356; PRO265; PRO941; PRO10905; PRO6003; PRO6004; PRO530; PRO5006; PRO500
                                                                 GENENTECH
                                                                                                  99WO-US20594
99WO-US21090
99WO-US21547
99WO-US28313
99WO-US28301
99WO-US28550
2000WO-US204341
2000WO-US04341
2000WO-US04341
2000WO-US04341
2000WO-US05437
2000WO-US054414
2000WO-US054414
2000WO-US054414
2000WO-US05841
2000WO-US05841
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2000WO-US05841
2000WO-US05841
2000WO-US05841
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                           Baker
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99WO-US20111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0139695
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161..167
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/note=
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127..131
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     Gao
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       Botstein DA,
W, Gerber H,
       Desnoyers
Gerritsen
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       ÄΕ,
     Eaton DL;
Goddard
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RESULT
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Matches 14
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                                                                                                                                                                                                                 Human; TR10 receptor; cytostatic; immunosuppressive; neuroprotective; antiinflammatory; anti-HIV; antiparkinsonian; nootropic; cardiant; vasotropic; antiallergic; antidiabetic; vulnerary; ophthalmological; antiviral; antipacterial; antifungal; antiparasitic; gene therapy; tumour necrosis factor receptor; cancer; leukaemia; autoimmune disorder; appoptosis; cardiovascular disorder; inflammatory disease; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a PRO polypeptide which is a transmembrane polypeptide is useful for gene therapy and identification of related polypeptides -
                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                     19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                             AAB50892 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                       28-MAY-1999;
07-JUL-1999;
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                                                                                                                                                                         Homo sapiens
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                             15-JUL-1999;
                                                                                    26-MAY-2000;
                                                                                                                                                                                                      infection;
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HUMAN
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                                                                                                                                                                                                      neurological
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Zhang Z;
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                                                                                    2000WO-US14554.
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GENOME
                          99US-0136786.
99US-0142563.
99US-0144023.
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SCI INC
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Pred. No.
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Tumas D, Watanabe CK, Will
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5. 4.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding a tumor necrosis factor receptor 10, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders, and diseases and disorders associated with apoptosis -
                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 31485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present
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                     New isolated nucleic a
                                                            N-PSDB;
                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                       ABB68231;
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                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                           (PEKE ) PE CORP NY
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                                                             2001-656860/75.
DB; ABL12334.
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                                                                                                   JC,
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                                                                                                  Adams M,
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                                                                                                                                                    2000US-191637P
2000US-0614150
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100.0%;
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                                                                                                   PWD,
                      detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 4.5e-06;
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Matches
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02-MAY-2000;
09-JUN-2000;
        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of a polynucleotide comprises at least 15 nucleotides; or (b) a combination of the specification of the sequences.
 oligonucleotide of an oligonucle
                                                                                                Claim
                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the evelopment of ABC18737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                         29-JUL-1999;
27-AUG-1999;
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|vgiivliv 34
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8; Conser
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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llarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; diagnosis; antisense therapy;
comprises at least eotide comprising a
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T, Wakamatsı
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0; Mismatches
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A, Nagai K,
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э NO.
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, Otsuki
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                                                                                                                                                                                                                      Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy.
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           a combination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH93633 to AAH18742 represent human cDNAs sequences; AAH92446 to CC AAB95893 represent human amino acid sequences; AAH93629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                      21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
14-SEP-2000;
19-OCT-2000;
                                WPI; 200
N-PSDB;
                                                                      Zhao
                                                                                 Wang
                                                                                           Tang
                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance, peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
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                                                                                                                                                                                                                                                   26-DEC-2000;
                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM41810
                                                                                                                   (HYSE-)
                                                                                                                                            29-NOV-
                                                                                                                                                                                                                                                                           26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                 leukaemia.
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                                 2001-442253/47
DB; AAI60966.
                                                                   QA,
                                                                                                                                                                                                                                                                                                                         sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide
                                                                                                                                            2000;
                                                                                                                   HYSEQ
                                                                   Liu C
Wang z
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                         2000US-0488725.
2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-0663450.
2000US-0663191.
2000US-0663191.
2000US-06727344.
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                                                                 u C,
u P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                     2000WO-US34263
                                                                                                                    INC
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                                                                   Asundi V,
Wehrman T,
Goodrich F
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   6741.
                                                                                Chen R
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                                                                   en R, Ma
u C, Xue
Drmanac R
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                                                                  Y,
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RT;
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                                                                              Ren F,
Zhang
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                                                                                           Wang
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such as

Novel nucleic

acids and al nervous

polypeptides, u system injuries

useful

for

treating

disorders

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Best Local S
Matches 8
                                                                                                                             21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity chamchas: Immune system suppression, activity, chamchactic/Chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.N.S disorders.
Note: The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification.
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                      Zhao
                                            Tang
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                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM41811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM41811 standard; Protein;
                                                                    (HYSE-)
                                                                                             29-NOV-2000;
                                                                                                         14-SEP-2000;
19-OCT-2000;
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                                                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                                                  chemokinetic;
                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-2001
                                                                                                                                                                                                                                                                                                       leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
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mes 8; Conserv
                    QA,
TY
                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tmntspgt 22
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                                                                    HYSEQ INC.
                     Liu (
Wang 2
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
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                                                                                           2000US-048B725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0652191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                 1 C,
1 P,
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                  thrombolytic;
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                               Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO 6741; 10078pp;
                      Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8;
Pred. No.
                     Ŗ
                                Chen R,
Xu C,
                                                                                                                                                                                                                                                                                                                                                                                         6742.
                   hen R, Ma Y,
Xu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                 screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 5
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                                                                                                                                                                                                                                                                                                                 arthritis; inflammation;
                              Qian XB,
Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 272;
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                                            Ren F,
                                Zhang
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                                ۲
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RESULT 3
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Best Local
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                                                                                                                                                       22-AUG-1997;
14-MAR-1997;
09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI60967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TR6; tumour necrosis factor related receptor; human; treatment; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW76828 standard; Protein; 303
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                                                    Deen
                                                                                                                                                                                                                                                            23-DEC-1997;
                                                                                                                                                                                                                                                                                                                14-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                     EP870827-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transplant
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                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP
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                                                 KC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nmation; arthritis; septicaemia; autoimmune disease; restenosis; plant rejection; infection; ischaemia; brain injury; bone disease; respiratory disease syndrome; acquired autoimmune disease syndrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atherosclerosis; Alzheimers
                                                                                                                                                       97US-0916625.
97US-0041230.
97US-0853684.
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                                                 PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   "Partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for this patent did
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Start codon missing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
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WPI; 1998-523156/45

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RRESULT 3
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XX Tumc
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The invention relates to a human tumour necrosis receptor, TR6. TR6 can be expressed by standard recombinant met The TR6 polypeptides are useful for treating chronic and acute inflammation, rheumatoid arthritis, septicemia, autoimmune disers of inflammatory bowel disease, psoriasis), transplant reject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour necrosis factor; TNF; TNF related receptor; TR6; human; antiinflammatory; immunosuppressive; cerebroprotective; vasotropic; antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic; nootropic; neuroprotective; antiarthritic; antirheumatic; antiischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor, TR6. TR6 polypeptides and polynucleotides can be used in the treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome, acute respiratory disease syndrome, restenosis, brain injury, (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                              polypeptides useful for e.g. for treating chronic inflammation, arthritis, septicemia, autoimmune di
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                                                                                                                                                                                                                                                                                                                   tumor necrosis factor related receptor TR6 polynucleotides
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8; Conserv
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                                                                                                                                                                                      Page 16-17; 47pp; English.
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Pred. No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; DR5; DR5s; TRAIL-R3; apoptosis related condition; cancer; thera autoimmune disease; viral infection; degenerative disorder; amyotrophic lateral sclerosis; retinitis pigmentosa; isohaemic injury; cerebellar degeneration; myelodysplastic syndrome; splice variant.
                                                                                                                                                                Newly isolated polynucleotide encoding a mammalian TRAIL receptor protein - useful in for screening for (ant)agonists that modulate the apoptotic activity mediated by DR5 or TRAIL-R3 proteins
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                                                                                                                                        Claim 16; Fig 5;
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ilarity 100.0%;
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This sequence is the human TRAIL receptor DR5s of the invention. An antibody against the TRAIL receptors is useful for detecting mammalian DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins. (Ant)agonists identified by the assay are useful for modulating the apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis related conditions which are treated in this way, include cancer (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis), viral infections

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This is the amino acid sequence of Tango-63e, a new member of the human tumour necrosis factor receptor superfamily. It was deduced from a human prostate cDNA clone sequence (see AAV62673). Two different forms of Tango-63, i.e. Tango-63e and Tango-63d (see AAW79260), have been identified. These are identical with the exception of the deletion of amino acids 183-211 of Tango-63d in Tango-63e. The invention also encompasses nucleic acid molecules encoding Tango-63d and -63e, vectors containing these nucleic acid molecules cells harboring recombined DNA encoding Tango-63d and/or -63e, transgenic animals that express Tango-63d and/or -63e, and recombinant knockout animals that fail to express Tango-63d and/or -63e. Methods are provided for the diagnosis and treatment of disorders associated with either an abnormally high or an abnormally low rate of apoptotic cell death. Inhibitors can be used for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated tumour necrosis factor related proteins - used to develop products for the diagnosis and treatment of apoptosis-related disorders, e.g. cancers, autoimmune disorders or neurodegenerative
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  autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₹
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Pred. No
(e.g. systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related
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RESULT 37
AAW76827
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    Matches
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Best Local
                                                                                                                                                                                                                                                                              22-AUG-1997;
14-MAR-1997;
09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  including AIDS, autoimmune diseases such as rheumatoid arthritis, and type I diabetes, septic shock, cerebral malaria, graft rejection, cytotoxicity, cachexia, and inflammation can be treated by altering the expression or activity of the polypeptides. The products can also be used for detection, diagnosis and screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    herpesviruses, poxviruses, and adenoviruses). Agonists can be used for treating e.g. neurodegenerative diseases, e.g. Alzheimer's disease, amyotrophic lateral sclerosis (ALS), Huntington's disease, retinitis plymentosa, spinal muscular atrophy, various forms of cerebellar degeneration, anaemia, myelodysplastic various forms of cerebellar degeneration, anaemia, myelodysplastic
receptor, TR6. TR6 polypeptides and polynucleotides can be used in treatment of chronic and acute inflammation, arthritis, septicaem: autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restenosis, brain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome, ischemic injury, myocardial infarction, cerebral ischemia or toxin-induced injury. In addition, T cell mediated diseases,
                                                           This sequence receptor, TR6.
                                                                                                                                                                                                                       Deen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TR6; tumour ne inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                               DNA encoding polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                   EP870827-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation; arthritis; septicaemia; autoimmune disease; restenosis; transplant rejection; infection; ischaemia; brain injury; bone disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TR6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW76827 standard;
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                                                                                                     Claim
                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 SPEMCRKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune-mediated glomerulonephritis), and viral infections
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                                                                                                                                                                                         1998-523156/45.
                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour necrosis
                                                                                                     ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory disease syndrome; acquired autoimmune disease syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
                                                                                                                                                                             AAV63094.
                                                                                                  Page
                                                                                                                                                                                                                      Young PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                               antibody, agonist,
                                                                                                                                                tumour necrosis factor receptor TR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102
                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis; Alzheimers
                                                                        represents a novel human tumour necrosis factor
                                                                                                     27-29;
                                                                                                                                                                                                                                                                              97US-0916625.
97US-0041230.
97US-0853684.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.4%;
                                                                                                  34pp;
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                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                               antagonist,
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                                                                                                                               etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human;
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                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment; stroke;
                                                                                                                                              corresponding
                                             septicaemia,
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brain injury

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RESULT :
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                    neurodegeneration; systemic lupus erythematosus;
glomerulonephritis; rheumatoid arthritis; graft rejection;
gsteoarthritis; psoriasis; septicaemia; inflammatory bowel disease;
Alzheimer's disease; Parkinson's disease; retinitis pigmentosa;
amyotrophic lateral sclerosis; aplastic anaemia; ischaemia;
                New isolated death domain containing receptor 5 - used to products for treating e.g. cancers, autoimmune disorders, infections, inflammation, graft-versus-host disease or
                                                                                                                                                                                                                                                                                                                                                                                                                 Death domain containing receptor 5; DR5; human; apoptosis; tumour necrosis factor receptor; cancer; autoimmune disease; inflammation; infection; AIDS; graft versus host disease;
          neurodegenerative
                                                                                   Gentz
                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                      29-JUL-1997;
17-MAR-1997;
                                                                                                                                                 17-MAR-1998;
                                                                                                                                                                    24-SEP-1998
                                                                                                                                                                                     W09841629-A2
                                                                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     diagnosis
                                                                                                                                                                                                                                                                                                                                                               septic
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW79083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW79083 standard; Protein; 411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative disorders), atherosclerosis and Alzheimers disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 spemcrkc 156
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                                                       1998-531568/45.
DB; AAV61469.
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                                                                                                                                                                                                                                                                                                                                                              shock;
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                            cachexia; anorexia; agonist; antagonist; therapy;
                                                                                                                     97US-0054021.
97US-0040846.
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                                                                                                                                                 98WO-US05377
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                            'label= Extracellular
                                                                                                                                                                                                                                                                              'label= Mat_protein
          disorders
                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%;
                                                                                                                                                                                                                         Intracellular
                                                                                                                                                                                                        Death
                                                                                                                                                                                                                                          Transmembrane
                                                                                                                                                                                                                                                                                               Sig_peptide
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                                                                                  uS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor 5 (DR5).
                                                                                  ΊY,
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                           develop
viral
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PRR PRR
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CC This is the amino acid sequence of human death domain containing CC receptor 5 (DR5), deduced from an isolated DR5 nucleic acid (see CC AAV61469). DR5 is a novel member of the tumour necrosis factor (CC AAV61469). DR5 is a novel member of the tumour necrosis factor (CC AAV61469). DR5 is a novel member of the tumour necrosis factor (CC AAV61469). DR5 is a novel member of the tumour necrosis factor (CC AAV61469). DR5 is a novel member of the tumour necrosis factor (CC AAV61469). DR5 is a novel member of the tumour necrosis factor (CC AAV61469). DR5 is a novel member of the tumour necrosis factor (CC AAV61469). DR5 is a novel member of the tumour necrosis factor (CC AAV61469). DR5 polypeptides is It shows homology to human (CC TNFR1), FAS and DR3. DR5 CDNA has been identified in primary (CC dendrinitie cells, endothelial tissue, spleen, chronic lymphocytic dead in the recombinant production of DR5 polypeptides. (CC e.g. the extracellular transmembrane, intracellular domains, cells and the combinant methods of producing (CC e.g. the extracellular transmembrane (CC domain; vectors, host cells and recombinant methods of producing the polypeptides are claimed. DR5 polypeptides can be used to identify agonists and antagonists, and to raise antibodies. (CC the polypeptides are claimed. DR5 polypeptides can be used to treat diseases DR5 mediated signalling, can be used to treat diseases by inflammation, graft versus host disease, acute graft (CC rejection, chronic graft rejection, rheumatoid arthritis) and (CC disease). Antagonists, which decrease DR5 mediated signalling, can be used to treat diseases, anyotrophic lateral sclerosis, retinitis, (CC parkinson's diseases, amyotrophic lateral sclerosis, retinitis, (CC parkinson's disease, amyotrophic lateral sclerosis, retinitis, (CC pickexia and anorexia. The products can also be used for detection, (CC cancersia and drug screening.) isohemic injury, toxin-induced (CC cancersia and anorexia. The products can also be used for detection, (CC cancersia and anorexia. The pro
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AAW93608 RESULT Matches Best Query Match WO9902653-A1 Killer protein; adriamycin inducible; human; p53-inducible; apoptosis-mediating activity; Human killer adriamycin-inducible protein. AAW93608; AAW93608 standard; Protein; 411 Homo sapiens neoplastic disease 18-JUN-1999 149 95 Local 39 SPEMCRKC 102 spemcrkc Similarity 8; Conserv Conservative (first entry) 156 3.4%; 0, Score 8; Pred. No. Mismatches . DB 19; chromosome
treatment; 0; Length 411 Indels animal model; 8p21; diagnosis; 0, Gaps 0

11-MAR-1998; 11-JUL-1997; 04-AUG-1997; 30-SEP-1997;

98US-0077661. 97US-0052305. 97US-0054710. 97US-0060473. 21-JAN-1999. 10-JUL-1998;

98WO-US14495

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RESULT 4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormality; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis-mediating activity and comprises an amino-terminal extracellular receptor, transmembrane and death domains. The nucleic acid molecule which encodes the protein, it's encoded signal transduction protein and antibodies of the invention are useful in the diagnosis and treatment of neoplastic diseases. The invention is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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11-MAR-1998;
                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apoptosis; human.
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N-PSDB; AAX23721.
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  New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
                                                                                                                                                                                                                                                                                           05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1999
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                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
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                                                                                                         1999-205191/17
DB; AAX23410.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             located on chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production of animal model systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           describés a novel human adriamycin-inducible killer
don chromosome 8p21, which also has p53-inducible,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0077526
98US-0077628
                                                                                                                                                                                                                                                                                         97US-0924634
                                                                                                                                                                                                                                                                                                                                            98WO-US18393.
usis and treatment of prostate cancer and gestational abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Ma
Best Loc
Matches
             Newly isolated polynucleotide encoding a mammalian TRAIL receptor protein - useful in for screening for (ant)agonists that modulate the apoptotic activity mediated by DR5 or TRAIL-R3 proteins
                                                                                                                                                                                                                                                                                                                                                           Human; DR5; DR5s; TRAIL-R3; apoptosis related condition; cancer; therapy; autolimmune disease; viral infection; degenerative disorder; amyotrophic lateral sclerosis; retinitis pigmentosa; ischaemic injury; cerebellar degeneration; myelodysplastic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DR5 protein sequence
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                                                                                  N-PSDB;
                                                                                                                                  Alnemri ES;
                                                                                                                                                                                                 15-AUG-1997;
                                                                                                                                                                                                                                14-AUG-1998;
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                                                                                                                                                                                                                                                                                             WO9909165-A1
                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                               (IDUN-) IDUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 spemcrkc
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                                                                                1999-181035/15
DB; AAX27279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
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                                                                                                                                                               PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2:
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                                                                                                                                                                                                 97US-0055906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Pred. No.
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AAW88410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis), viral infections (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral sclerosis, retinitis plymentosa, cerebellar degeneration, myelodysplastic syndromes (e.g. aplastic anaemia) and ischaemic hjury (e.g. myocardial infarction and stroke). The polynucleotides can also be used to treat these diseases. Antisense oligonucleotides to the DNA sequences can be used to form a composition that is useful for inhibiting expression of a human DR5 or TRAIL-R3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the human TRAIL receptor DR5 of the invention. An antibody against the TRAIL receptors is useful for detecting mammalian DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins. (Ant)agonists identified by the assay are useful for modulating the apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis related conditions which are treated in this way, include cancer
                       23-DEC-1998
                                                                           WO9858062-A1
                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegeneration; autoimmune disease; inflammation; cancer; apoptosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo-2 ligand; Apo-2DcR; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Apo-2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW88410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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| 149 spemcrkc 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 SPEMCRKC 102
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                            138..179
/note= "cysteine-rich
                                                                                                                                                                                                                                                                                                                               96..137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                  'note= "death domain'
                                                                                                                                                 'label= Met, Leu
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100.0%; Pr
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                                                                                                                       "encoded by WTG
                                                                                                                                                                                                                                                                                                  "cysteine-rich region"
                                                                                                                                                                                                                                                                                                                                                      "intracellular
                                                                                                                                                                                                                                                                                                                                                                                                  "transmembrane domain"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour necrosis factor receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                      domain"
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RESULT AAW83321
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produced from overlapping cDNA clones obtained from human kidney and pancreatic cDNA libraries. The invention relates to Apo-2DoR (see AAW88408), a novel member of the tumour necrosis factor receptor family that binds to Apo-2 ligand and is involved in apoptosis. Apo-2DcR polypeptides are used to modulate apoptosis of mammalian cells (claimed) e.g. in the treatment of neurodegeneration, autoimmune diseases and inflammation. The Apo-2DcR polypeptides are optionally used in conjunction with Apo-2 ligand, the bloavablability of which is increased by antibody-mediated blockade
                    09-FEB-1998;
15-MAY-1997;
                                                                                                                                                                                                                 TNF
                                                                                                                                                                                                                           Human; Apo-2; receptor; apoptosis; neurodegenerative disease; tumour necrosis factor; TNF; tumour necrosis factor receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Apo-2DcR polypeptide - used for modulation and diagnosis of apoptosis, e.g. in neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-095340/08.
N-PSDB; AAV84352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashkenazi AJ,
Kim KJ, Wood
                                                        14-MAY-1998;
                                                                                19-NOV-1998
                                                                                                       W09851793-A1
                                                                                                                                                      Misc-difference
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                             Human Apo-2 protein
                                                                                                                                                                                                                                                                                     16-MAR-1999
                                                                                                                                                                                                                                                                                                            AAW83321;
                                                                                                                                                                                                                                                                                                                                  AAW83321 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises human Apo-2 ligand. The amino acid sequence was deduced from a nucleotide sequence (see AAV84352)
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8; Conserv
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WI;
                    98US-0020746.
97US-0857216.
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                                                        98WO-US09704
                                                                                                                                                      Location/Qualifiers 410
                                                                                                                              /note=
                                                                                                                                           'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%;
                                                                                                                              "encoded by WTG"
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                                                                                                                                                                                                                            cancer;
TNFR;
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(GETH ) GENENTECH INC

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RESULT 4
AAB29790
PRESENTATION OF STREET PRESENTATION OF STREET
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAIL binding; TNF-related apoptosis-inducing ligand; pro-apoptotic; tumour necrosis factor receptor family; TNF; graft-versus-host disease; viral infection; cancer; leukaemia; immunodeficiency; autoimmune disease; T-cell mediated immune response; osteoarthritis; psoriasis; septicaemia; inflammatory bowel disease; parasitic infection; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Apo-2 polypeptide inducing apoptosis - useful to conditions linked with decreased apoptosis e.g. cancer,
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CC autoimmune disorder. The method comprises administering an antibody CC specific for human death domain containing receptor-5 (DR5); AAB29790) CC and a second agent selected from TRAIL (TNF-related apoptosis-inducing CC ligand), a tumour necrosis factor (TNF), a TNF blocking agent, an C immunosuppressive agent, an antibiotic, an antiinflammatory agent, a chemotherapeutic agent, or a cytokine. DR5 is a member of the TNF CC inmunosuppressive agent, and is a mediator of apoptosis, being able to CC bind TRAIL. The method of the invention is useful for the treatment of CC graft-versus-host disease, viral infection, cancer, leukemia, and condeficiency, or an autoimmune disorder. The DR5 antibody is useful for treating or preventing diseases and conditions associated with CC increased cell survival and/or insensitivity to apoptosis inducing agents. Examples of such diseases are solid tissue concers and CC leukaemias. Antagonists of DR5 are useful for inhibiting T-cell mediated immune responses such as graft-versus-CC associated with T-cell mediated immune responses such as graft-versus-CC host responses, and preventing and/or treating diseases and conditions associated with T-cell mediated immune responses such as graft-versus-CC bowel disease, autoimmune diseases and leukaemia. DR5 nucleotides and proteins are useful for disponsis, prevention and/or treatment of CC parasitic, bacterial, and viral infections, restenosis and autoimmune CC disorders. The present sequence represents human DR5.
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating graft-versus-host disease, viral infection, cancer, leukemia, immunodeficiency, or an autoimmune disorder comprising administering a antibody to Death domain containing receptor (DR5) and a second agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1A-B; 266pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel method for treating graft-versus-host disease, viral infection, cancer, leukaemia, immunodeficiency, or an
Sequence
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                                                                        polypeptide; immunization; antigen; polyclonal antibody;
lonal antibody; Apo-2L receptor; therapy; apoptosis; autoi
e-mediated cell death; neurodegenerative; inflammatory.
                                                                                                           Apo-2 polypeptide
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100.0%; Pred. No.
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Misc-difference

Location/Qualifiers 410

/note= "encoded by WTG" 1abel= unknown sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The invention provides a method for producing antibodies (Abs) by CC immunizing an animal with at least two different antigens. The method CC comprises: (a) immunizing an animal with at least two different antigens, CC comprises: (a) immunizing an animal with at least two different antigens, CC comprises: (a) immunizing an animal with at least two different antigens, CC comprises: (a) immuniciant and compressed to generate polyclonal Abs against each antigen in the animal; (b) CC preparing monoclonal Abs (MAbs) using immune cells of the above animal; CC and(c) screening the MAbs to identify one or more MAbs which bind to each cused for therapy. The Apo-2L receptor (ant)agonists and can be cused for therapy. The Apo-2L receptor Abs can be used for enhancing commune-mediated cell death in cells expressing Apo-2L receptors. CC Agonistic Abs which specifically cross-react with 2 or more different CC Apo-2L receptors can be used for inducing apoptosis in mammalian cancer cells. Antagonistic Abs can be used for blocking apoptosis, e.g. in neurodegenerative disease, or to block potential autoimmune/inflammatory celfects of Apo-2 resulting from NF-approx. Ha activation. The Abs can also be used for detection, diagnosis and affinity purification. The method con reduce the number of animals that need to be immunized and sacrificed in order to make 2 or more MAbs with differing antigen-binding constitutions. The method conference of the constant of the c
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cancer; tumour; apoptosis; lymphoma; blastoma; sarcoma; leukae
                                                                                                                                                                                                                                                                                 Human apoptotic protein, Apo-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of antibodies using 2 or more different antigens, used for producing antibodies against Apo-2 ligand receptors useful for inducing apoptosis, particularly in cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04038 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specificities. The present sequence represents
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a human Apo-2 p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC The sequence represents human Apo-2, an apoptotic protein used as an CC immunogen to make the monoclonal antibodies of the invention. The CC invention relates to an isolated antibody which specifically cross-reacts CC with two or more different Apo-2 ligand (Apo-2L) receptors. Apoptosis by CC monoclonal antibody 3H3.14.5 after crosslinking with anti-mouse Ig was CC tested. Human 9D cells in complete RPMI medium were added. Cells were CC incubated with the monoclonal antibody in 100 micro on ice for 15 CC minutes. Cells were then incubated with goat anti-mouse IgG FC complete RPMI medium overnight at 37 degrees C. After washing once with PBS, cells were resuspended in PBS containing 0.5% BSA and incubated with FITC-CC Annexin and propidium iodide for 15 minutes in the dark. Dead cells were detected by FACScan. The 3H3.14.5 antibody was able to inhibit apoptosis induced by interaction between Apo-2L and Apo-2. This antibody was further capable of inducing apoptosis of 9D cells in the presence of an CC inducing apoptosis in mammalian cancer cells for treating cancer CC including carcinoma, lymphoma, blastoma, sarcoma and leukaemia, and are useful in diagnostic assays for their antigen, e.g. detecting its CC expression in specific cells, tissues or serum and for affinity courification of antigen from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                            agonistic antibody; nuclear factor kappa B; NF-kappa-B activation; cancer; tumour: '... colon cancer: alian-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human monoclonal antibody for inducing apoptosis in mammalian cancer cells, specifically cross-reacts with two or more different Apo-2 ligand receptors -
                                                                                                                                               Human Apo-2 receptor;
Peptide
                                               Homo sapiens
                                                                                                                                                                              Human Apo-2 receptor precursor,
                                                                                                                                                                                                                25-JUN-2001
                                                                                                                                                                                                                                                AAB73442;
                                                                                                                                                                                                                                                                                 AAB73442 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 5; 29pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                               149 spemcrkc
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Location/Qualifiers
1..53
                                                                                                                                               caspase-dependent apoptosis induction;
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[00.0%; Pred. No.
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                                                                                                                                                                              SEQ ID NO: 2
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CC cells which express the Apo-2 receptor protein (AAB73442, AAB73443).

CC cells which express the Apo-2 receptor protein (AAB73442, AAB73443).

CC The method involves exposing the cells to an Apo-2 agonistic antibody,

CC which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor

CC (also referred to simply as Apo-2) is a member of the tumour

CC necrosis factor receptor (TNFR) family, and its natural ligand is the

CC Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able

CC to trigger caspase-dependent apoptosis, and is also able to activate

CC NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an

CC approximately 45 kD type I transmembrane protein, and contains a death

CC domain in the cytoplasmic region (residues 324-392). It exhibits

CC significantly more sequence identity to the apoptosis-linked receptor

CC The Apo-2 receptor agonist monoclonal antibodies used in the method of

CC the invention are 3F11.39-7, 3H3.14, 5, 3D5.1.10 and 3H1.18.10. The

CC method of the invention is used to induce apoptosis in Apo-2-expressing

CC cells, particularly cancer cells. It may therefore be used for treating

CC mammalian cancers, especially lung cancer, colon cancer and glioma.

CC in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing exposing Apo-2 ago
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF84481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis in mammalian cells for treating cancer, comprises mammalian cells or cancer cells expressing {\tt Apo-2} receptor,
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116..129
119..137
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96..13
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54..18;
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                                                                                                                                                                                                                                                                                                                                                                                                                           90pp;
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RESULT 48
AAB73443
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Best Local Similarity
Thehes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                     Human Apo-2 receptor; caspase-dependent apoptosis induction; programmed cell death; pro-apoptotic; death domain; agonistic antibody; nuclear factor kappa B; NF-kappa-B activation; cancer; tumour; lung cancer;
               14-SEP-2000;
                                                                                                                                        Disulfide-bond Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                 Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73443 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence differs from the human Apo-2 receptor precursor given in AAB73443 in that residue 410 of this sequence
                                                                        Misc-difference
                                                                                                        Domain
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                                                                                                                                                                               Disulfide-bond
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                                                                                                                                                                Domain
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                                                                                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 AA;
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                2000WO-US25436
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97
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/note= "Intracellular domain"
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112
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                                                                                                                                                                                                                                                                                "Mature human
                                                                                "Death domain"
                                                                                                                "Transmembrane domain"
                                                                                                                                                                                        "Binds
                                                                                                                                                                                                                               "Cysteine-rich pseudorepeat domain
                                                                                                                                                                                                                                                               "Extracellular domain. This domain is
                                                                                                                                                                                                                                                                                               "Signal peptide
                                                                                                                                                       "Cysteine-rich pseudorepeat
                                                                                                                                                                                                       "Binds Apo-2L'
                                                                                                                                                                                                                                                        alternatively residues
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Pred. No.
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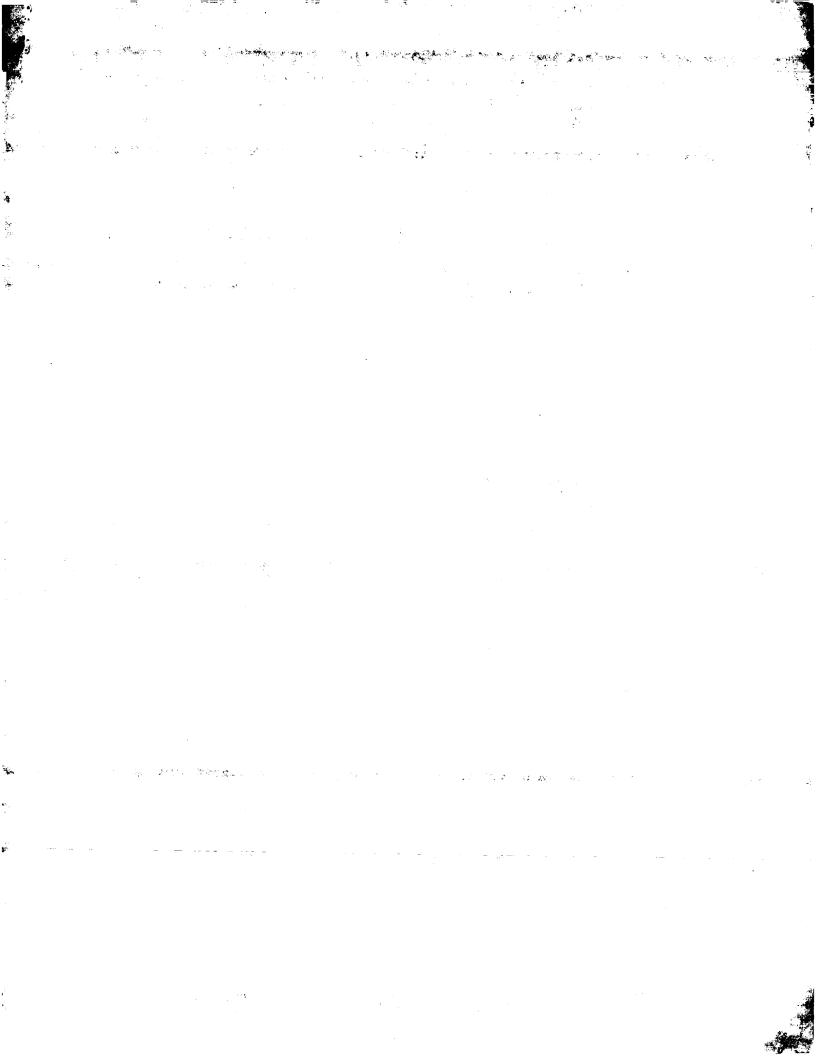
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for inducing apoptosis in mammalian CC cells which express the Apo-2 receptor protein (AAB73442, AAB73443). CC The method involves exposing the cells to an Apo-2 agonistic antibody, CC which induces Apo-2 receptor mediated apoptosis. The Apo-2 receptor CC consistence of the tumour concerns factor receptor (TNFR) family, and its natural ligand is the CC necrosis factor receptor (TNFR) family, and its natural ligand is the CC concerns factor receptor (TNFR) family, and its natural ligand is the CC to trigger caspase-dependent apoptosis, and is also able to activate CC NF kappa-B (nuclear factor Kappa B). The Apo-2 receptor is an approximately 45 kD type I transmembrane protein, and contains a death CC domain in the cytoplasmic region (residues 324-392). It exhibits considered the substitution of the apoptosis-linked receptor CC Significantly more sequence identity to the apoptosis-linked receptor CC CR which also binds Apo-2L, than other apoptosis-sosociated proteins. The Apo-2 receptor agonist monoclonal antibodies used in the method of the invention are 3F11.39.7, 3H3.14, 5, 3D5.1.10 and 3H1.18.10. The
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                          Key
Domain
                                                                                                                                         Tumour necrosis factor; TNF; TNF related receptor; TR6; human; antiinflammatory; immunosuppressive; cerebroprotective; vasotropic; antiasthmattc; anti-HIV; osteopathic; cytostatic; antiatherosclerotic; noootropic; neuroprotective; antiarthritic; antirheumatic; antiischemic
                                                                                                   Homo
                                                                                                                              gene
                                                                                                                                                                                                                   Human tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             method of the invention is used to induce apoptosis in Apo-2-expressing cells, particularly cancer cells. It may therefore be used for treating mammalian cancers, especially lung cancer, colon cancer and glioma. The present sequence represents human Apo-2 as given in figure 2A. Note: The present sequence differs from the human Apo-2 receptor precursor given in AAB73442 in that residue 410 of this sequence is Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inducing apoptosis in mammalian cells for treating cancer, comprises exposing mammalian cells or cancer cells expressing Apo-2 receptor, Apo-2 agonist antibody -
                WO200077191-A1
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                                                                                                                                                                                                                                                                           AAB48348
                                                                                                                                                                                                                                                                                                      AAB48348 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor given in AAB7 rather than Met or Leu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 2A; 90pp;
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                                                                                                   sapiens
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Similarity 100.0%;
8; Conservative
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Tumour necrosis factor; TNF; TNF related receptor; TR6; human; antiinflammatory; immunosuppressive; cerebroprotective; vasotropic; antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic; nootropic; neuroprotective; antiarthritic; antirheumatic; antiischemic gene therapy; vaccine; TNF-alpha; bone disease; cancer; fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    research reagents and materials for discovering treatments and diagnostics to animal and human diseases. The polypeptides may furth used as immunogens to produce antibodies immunospecific for the TR6 polypeptides. The polynucleotides may also be used as hybridization probes for cha and genomic DNA, for isolating full-length cDNAs and genomic clones encoding TR6 and of other genes having high sequence similarity to TR6 gene, and for chromosome identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This represents a human tumour necrosis factor (TNF) related receptor, TR6. TR6 can be expressed by standard recombinant methodology. The TR6 polypeptides are useful for treating chronic and acute inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft vs. host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, asthma, restenosis, brain injury, AIDS (acquired immunodeficiency syndrome), bone diseases, cancer, atherosclerosis, and Alzheimer's disease. These may also be used to inhibit production of TNF-alpha and eicosanoids, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumor necrosis factor related receptor TR6 polynucleotides polypeptides useful for e.g. for treating chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, infectional acute inflammation arthritis.
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein;
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                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumor necrosis factor related receptor TR6 polynucleotides and polypeptides useful for e.g. for treating chronic and acute inflammation, arthitis, septicemia, autoimmune diseases, infection cancer, bone diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyright
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2.1 100 2 PH1088 2.1 100 2 A12298 2.1 100 2 T41217 2.1 100 2 F86836 2.1 100 2 D22848 2.1 101 2 S07706	2.1 99 2 \$14585 2.1 99 2 \$14586 2.1 99 2 \$E69267 2.1 99 2 \$E82707 2.1 100 2 \$P\$1087	5 2.1 99 2 PH1089 5 2.1 99 2 SH4582 5 2.1 99 2 SH4583 5 2.1 99 2 SH4583 5 2.1 99 2 SH4584	5 2.1 98 2 S55622 5 2.1 98 2 H81072 5 2.1 98 2 S72990 5 2.1 98 2 S26981 5 2.1 98 2 T29026	5 2.1 97 2 \$72866 5 2.1 97 2 \$725342 5 2.1 97 2 \$72576 5 2.1 97 2 \$785981	5 2.1 97 2 B90725 5 2.1 97 2 C91136 5 2.1 97 2 B86506 5 2.1 97 2 F64809	5 2.1 97 2 F65108 5 2.1 97 2 S60889 5 2.1 97 2 G72117	5 2.1 96 2 F97645 5 2.1 96 2 AD2869 5 2.1 97 2 PH1090	5 2.1 95 2 T25253 5 2.1 96 1 JU0349 5 2.1 96 1 ERBPGZ 5 2.1 96 2 T17865	5 2.1 94 2 H70654 5 2.1 94 2 A69105 5 2.1 94 2 C97181 5 2.1 95 2 T06905	5 2.1 93 2 \$04157 5 2.1 93 2 \$33842 5 2.1 93 2 \$C0592 5 2.1 93 2 \$B6305	5 2.1 93 2 \$50649 5 2.1 93 2 \$6764 5 2.1 93 2 \$84175	5 2.1 92 2 1/1151 5 2.1 92 2 885911 5 2.1 93 2 \$77812	5 2.1 92 2	5 2.1 91 2 F83654 5 2.1 92 2 A84637 5 2.1 92 2 75348	5 2.1 91 2 83469 5 2.1 91 2 83469 5 2.1 91 2 F59093	5 2.1 91 2 E81715 5 2.1 91 2 H86701 5 2.1 01 2 B86526	5 2.1 91 2 G71562 5 2.1 91 2 G72088	5 2.1 90 2 5 2.1 90 2 5 2.1 91 1	5 2.1 89 2 5 2.1 90 1	5 2.1 89 2 5 2.1 89 2
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C;Geneti
A;Gene:
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
                            RESULT
G86566
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R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwoc Nature Genet. 21, 385-389, 1999
  transcription termination C; Species: Chlamydophila r
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A;Experimental source: strain AR39, HL cells
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A; Residues: 1-464 < REA>
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Best Local
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pneumoniae, Chlamydia
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0; Mismatches
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B347870
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                                                B. subtilis YbtB protein homolog lin0882 [imported] - Listeria innocua (strain C;Species: Listeria innocua (c;Species: Listeria innocua (c;Species: Listeria innocua (c;Species: C?-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AB1543 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
A; Authors: Kreft, J.; I ok, C.; Schlueter, T.;
                         Science 294, 849-852,
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Kurapkat, G.;

Tierrez,

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Vazquez-Boland,

Madueno, E.; Boland, J.A.;

Maitournam, Voss, H.; W

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C:Species: Listeria monocytogenės
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change
C:Accession: ACILB5
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero,
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R/Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuch Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences A;Reference number: A66491; MUID:20330349
A;Accession: G86566
A;Status: preliminary
                                                                                                                                                                     A;Gene: lmo0883 C;Superfamily: Bacillus subtilis hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
A;Title: Comparative genomics of Listeria species.
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Science 294, 849-852, 2
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A; Experimental source: strain J138
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A; Residues: 1-491 <GLA>
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A; Accession: AC1185
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C;Accession: G86566
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s; Pred. No. 3.9
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RESULT 6
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hypothetical protein ZK84.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
C; Accession: T29018
R; Kirsten, J.
submitted to the EMBL Data Library, April 1995
submitted to the sequence of C. elegans cosmid ZK8
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A; Residues: 1-685 < CAR>
A; Cross-references: GB:AL162752;
A; Experimental source: serogroup
C; Genetics:
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A; Residues: 1-494 <GLA>
A; Cross-references: GB:AL592022; PIDN:CAC96114.1;
A; Experimental source: strain Clip11262
C; Genetics:
A; Experimental source:
C; Genetics:
A; Gene: CESP: ZK84.1
A; Map position: 2
                                                                              A; Molecule type: DNA
A; Residues: 1-801 <KIR>
A; Cross-references: EMBJ
                                                                                                                                                           A; Description: The sequence A; Reference number: 220553 A; Accession: T29018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: metG; NMA0275
C;Superfamily: methionine--tRNA ligase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete DNA sequence of a serogroup A;Reference number: A81775; MUID:20222556 A;Accession: G82022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1543
A;Status: preliminary
                                                                                                                                    A; Status: preliminary; translated
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Nature 404, 502-506, 2000
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C;Superfamily:
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nes 8; Conserv
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                                                          EMBL:U23181; PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZK84.1 
be: strain Bristol N2; clone ZK84
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100.0%;
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A, strain Z2491
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Rajandream,
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R; Kershaw, J.
submitted to the EMBL Data
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A;Gene: CESP:F23H12.3
A;Map position: 5
A;Introns: 22/3; 56/3; 95/3
C;Superfamily: Caenorhabditis elegans hypothetical
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A; Residues: 1-155 <GRE>
A; Cross references: EMBL: X91961; NID: g1107494;
A; Cross references: EMBL: X91961; NID: g1107494;
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Best Local Similarity
"---hes 8; Conserv."
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A;Experimental source: clone F23H12
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C;Date: 15-Oct-1999 #sequence_revision
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  hypothetical C; Species: S
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A; Residues: 1-165 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F23H12.3 - Caenorhabditis elegans
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Best Local S
Matches 7
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Best Local
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al protein SSO2176 [imported] - Sulfolobus solfataricus
                                                                                                                                  Similarity 7; Conserv
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                Sulfolobus solfataricus
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Decliphering the biology of Mycobacterium A;Reference number: A70500; MUID:98295987 A;Accession: D70519 A;Status: preliminary; nucleic acid sequence not s A;Molecule type: DNA
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H72242
C:Species: Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: H72242
                                                                                                                                                                         probable lppC protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 2
C;Accession: D70519
                                                                                                      Rajandream, M.A.; Ro
Nature 393, 537-544,
                                                                                                                                       R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
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A;Cross-references: GB:AE001800; GB:AE000512; NID:g4982090; PIDN:AAD36607.1; PID:g49821
A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316
A;Accession: H72242
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C; Accession:
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A; Residues: 1-199 <ARN>
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A; Gene: SSO2176
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A;Accession: H90386
A;Status: preliminary
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A;Description: Sulfolobus solfatarious complete genome
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A; Residues: 1-184 < KUR>
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Matches 7
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7; Conserv
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44, 1998
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                                                                                                                       Seeger, K.; Skelton, S.; Squares,
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; Pratt, M.S.;
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                                                                    Whitehead, S.; Barrell, B.G tuberculosis from the comple
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                   translation
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X.; Thi-Ngoc, H.P.;
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                                                                                                                                                       Gordon,
                                                                    genome
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Q
                                                                                                                     C;Genetics:
A;Gene: paf93
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A; Map position: 1
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                                Query Match
Best Local S
Matches 7
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
 149 PAPAAEE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 TPAPAAE
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A;Residues: 1-201 <COL>
A;Cross-references: GB:Z97193; GB:AL123456; NID:g3261816; PIDN:CAB10030.1; PID:e32482
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: lppC
                                                                                                                                                                                         Plant Sci. 105, 71-80, 1995
A;Title: Characterization of two barley genes that respond A;Reference number: 215371
A;Accession: T05958
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                       cold acclimation protein homolog - barley
C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
                                                                                                                          A; Experimental source:
                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-255 < GRO>
                                                                                                                                                                                                                                                                                    R; Grossi, M.; Gulli,
                                                                                                                                                                                                                                                                                                       C; Accession: T05958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896 A;Accession: E75477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; U.S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE001932; A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-219 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 GTPAPAA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 GTPAPAA 153
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n 3.0%;
Similarity 100.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100 7; Conservative
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                                                                                                                          EMBL:X84056; NID:g642245; PIDN:CAA58875.1; pe: cv. Georgie, leaf
                                                                                                                                                                                                                                                                                    M.; Stanca, A.M.; Cattivelli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.0%;
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Score 7; DB 2; ; Pred. No. 26; 0; Mismatches
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   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE000513;
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Pred. No.
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23;
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21;
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L.; Utterback,
   Indels
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                                                                                                                                                                                                                                                    rapidly to dehydration
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                                                                                                                                             PID: g642246
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   0;
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T.; Zalewski,
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrar, las Neto, E.; Docenha, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000
A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martths, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; M.C.; de Oliveira, M.C.; de Oliveira, R.C.; Palmierl, D., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Santelli, R.V.; Sawasa, A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-256 <SIM>
A; Residues: 1-256 <SIM>
A; Residues: 1-256 <SIM>
A; Cross-references: GB: AE003987; GB: AE003849; NID: g9106634; PIDN: AAF84400.1; GSPDB:
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carr
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carr
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Farreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.;
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.;
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marti
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein xF1591 [imported] C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision C;Accession: B85661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; anonymous, The Xy16
Nature 406, 151-157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-256 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
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%; Pred. No. 26;
0; Mismatches
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26;
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          M.V.; Martins,
C.; Miyaki, C.Y
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PAPAAEE

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#text\_change

14-May-1999

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A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A;Conetics: annotation
                                                                                                                                                                                                                                                                                                 C;Geneti
A;Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
B82648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The genome sequence of the plant pathogen Xylella A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;anonymous, The Xylella fastidiosa Nature 406, 151-157, 2000
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A;Cross-references: GB:AE003994; GB:AE003849;
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uthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
"Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
149 PAPAAEE
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red. No. 26;
Mismatches
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26;
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A;Gene:
A;Map po
                                                                                                                                          A;Title: Multiple chromosomes in bacteria. The Yin A;Reference number: Z24108; MUID:99442363 A;Accession: T46853 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                             C; Accession: T46853
R; Mackenzie, C.; Simmons, A
Genetics 153, 525-538, 1999
                                                                                                                                                                                                                                                             yibQ protein [imported] - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
                                                                                                   A; Molecule type: DNA
A; Residues: 1-266 < MAC>
A; Cross-references: EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T15453
hypothetical protein C08A9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T15453
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-262 <KAL>
A;Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193303
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                  RESULT 19
T46853
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                                                                                  A; Experimental source: strain
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A; Introns: 45/3; 79/3; 128/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-263 <LAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, December 1995 A; Description: The sequence of C. elegans cosmid C08A9 \,
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A; Introns: 6/2; 68/3; 121/1; 163/3; 226/1
A; Note: T14P8.5
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ilarity 100.0%;
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                                                                                   EMBL:AF108766; NID:g4185542; PIDN:AAD09126.1; re: strain 2.4.1
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100.0%; Pred. No.
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Pred. No. 27;
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C; Keywords:
                             moaB protein [imported] - Agrobacterium tumefaciens plasmid pTil5955 C;Species: Agrobacterium tumefaciens C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-J. C;Accession: T45537
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T45537
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               R;Lyi,
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R;Guilfolie, P.G.; 1
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T06802
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A; Residues: 1-283 <GUI>
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A; Residues: 1-268 < DAN>
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             S.M.; Jafri,
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S.; Winans, S.
339-347, 1999
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submitted to the EMBL Data A,Description: A bacterial A;Reference number: S27706 A;Accession: S27708 A;Status: preliminary
                                                                               A;Cross-references: EMBL:M73758; NID:g153228; PIDN:AAA74718.1; PID:g153231
C;Superfamily: Streptomyces peucetius daunorubicin resistance protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                      daunorubicin resistance protein - Streptomyces peucetius
C;Species: Streptomyces peucetius
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T06802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U73210; NID:g1657842; PIDN:AAB18201.1; A;Experimental source: cv. Norstar; seedling; shoot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cold acclimation protein WCOR410b - wheat
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Best Local
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                 3.0%;
100.0%;
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100.0%; Pred. No.
                                                                                                                                                                                                                      Library, August 1991 analog of the mdr gene of mammalian
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                 Score 7;
Pred. No.
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Pred. No.
 Mismatches
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        DB
28;
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0;
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18-Feb-2000 #text\_change 21-Jul-2000

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C;Accession: F8182b
R;Parkhill, J.; Achtman, M.; James,
R;Parkhill, J.; Jagels, K.; Leather,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B A;Reference number: A81000; MUID:20175755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
C81050
                                                                                                                                                                                                                                                  probable cytochrome c NMA1977 [imported] - Neisseria meningitidis (strain 22491
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome c oxidase, chain III NMB1723 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: C81050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Mannopinic acid and agropinic acid catabolism A;Reference number: Z23002; MUID:99141607 A;Accession: T45537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-365 <TET>
A;Cross-references: GB:AE002522; GB:AE002098; NID:g7226972; PIDN:AAF42068.1;
A;Experimental source: serogroup B, strain MC58
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C;Superfamily: oligopeptide
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A; Residues: 1-313 <LYI>
                                                                                                                   A; Title: Complete DNA sequence A; Reference number: A81775; MU: A; Accession: F81826
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   A;Experimental source:
C;Genetics:
               A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85197.1; PID:g738060A;Experimental source: serogroup A, strain Z2491
                                                         A; Molecule type: DNA
A; Residues: 1-365 < PAR>
                                                                                               A; Status: preliminary
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Best Local S
Matches 7
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Best Local S
Matches 7
                                                                                                                                                                    ;Parkhill, U.,
Holroyd, S.; Jagels, K.;
402-506, 2000
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Conservative 0;
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llarity 100.0%;
Conservative (
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%; Pred. No. 35;
0; Mismatches
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3; Pred. No. 31;
0; Mismatches
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                                                                                                                                                                                          K.D.; Bentley,
S.; Moule, S.;
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                                                                                                                                                                                          S.D.; Churcher, C.;
Mungall, K.; Quail,
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M.A.;
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Dougherty,
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                                                                                                                                                                                          S.R.; More.
Rajandream,
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erty, B.A.
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A;Map pc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T01169

R;Takabatake, R.; Hata, S.; Taniguchi, M.; Kouchi, H.; submitted to the EMBL Data Library, July 1998

A;Description: Isolation and Characterization of cDNAs A;Reference number: Z14251

A;Accession: T01169
                                                                                                                                                                                                                                                                                                                                                       C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision
C;Accession: T50265; T38158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphate transport protein, mitochondrial - maize
C;Species: Zea mays (maize)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999
                                                     A; Molecule type: DNA
A; Residues: 229-374 <DEV>
A; Residues: 229-374 <DEV>
A; Cross-references: EMBL: 270043; NID: 91220275; PIDN: CAA93888.1;
A; Experimental source: strain 972h-; cosmid c22E12
                                                                                                                                submitted to the EMBL Data Library, A; Reference number: Z21775 A; Accession: T38158
                                                                                                                                                                                     A;Cross-references: EMBL:AL133498; PIDN:CAB63500.1; GSPDB:GN00066; SPDB:SPAC890.09
A;Experimental source: strain 972h(-); cosmid c890
R;Deylin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
                                                                                                                                                                                                                                                                                                                     R; Saunders, D.; Harris, D.; submitted to the EMBL Data I
                                                                                                                                                                                                                                                                                                                                                                                                  probable phosphate/phosphoenolpyruvate translocator C;Species: Schizosaccharomuros rombo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: NMA1976; NMA1977
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A; Residues: 1-258 <SAU>
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A; Residues: 1-366 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated
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A; Accession: T50265
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Best Local
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Best Local
                                     Genetics:
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position:
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                 SPAC22E12.01;
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                 SPDB:SPAC890.09
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                                                                                                                                                                                                                                                                                                                   ; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. Library, December 1999
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%; Pred. No. 35;
0; Mismatches
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Pred. No.
                                                                                                                                                                       March 1996
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35;
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                                                                          GSPDB:GN00066; SPDB:S
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                                                                                                                                                                                                                                                                                                                                                                                                                    (Schizosa
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Similarity 7; Conserv

Conservative

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3.0%;

Score Pred.

red. No. 36; Mismatches

0;

Indels

0;

Gaps

0

ຸນ

Length 374;

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hypothetical protein PH0703 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000 C;Accession: H71116 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamot
                                                                                     RESULT
H71116
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Yoo, C.J.; Wolin, S.L.
Mol. Cell. Biol. 14, 5412-5424, 1994
A;Title: La proteins from Drosophila melanogaster
A;Reference number: A53781; MUID:94309661
A;Accession: A53781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 28
A53781
ribonucleoprotein La - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Sep-1999
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                                                                                                                                                                                                                                                                                                        A;Cross-references: FlyBase:FBgn0011638
C;Superfamily: ribonucleoprotein La; ri
C;Keywords: RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: FlyBase:FBgn0011638
C;Superfamily: ribonucleoprotein La; ri
C;Keywords: leucine zipper; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-390 <BAID
A;Cross-references: GB:U07652; NID:g464019;
                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references:
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A; Residues: 1-390 < YOO>
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A;Title: Developmental characterization of
A;Reference number: A53773; MUID:94309632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Bai,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             La/SS-B homolog D-la - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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A53773
La/SS-B homolog
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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Best Local
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Best Local
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                                                                                                                                                         PAPAAEE
                                                                                                                                                                                                                         Similarity 7; Conserv
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                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           GB:L32988;
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Pred. No. 37;
0; Mismatches
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Pred.
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No.
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37;
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37;
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                                                                                                                                                                                                                                                       Length 390;
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A; Gene: CESP:F28
A; Map position:
A; Introns: 28/3;
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R; Wall,
                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F28G4.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T21515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-431 <MIC>
A; Cross-references: EMBL: X87847; NID: 9871007; PIDN: CAA61121.1; |
C; Superfamily: ornithine decarboxylase
C; Keywords: carbon-carbon lyase; carboxy-lyase; phosphoprotein;
F; 94/Binding site: pyridoxal phosphate (Lys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ornithine decarboxylase (EC 4.1.1.17) - jimsonweed (FC 4.1.1.17) - jimsonwe
                                                                                      A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                              submitted to the EMBL Data A; Reference number: Z19433 A; Accession: T21515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Molecular cloning and functional A;Reference number: S64704; MUID:96195135 A;Accession: S64704
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A;Title: Complete sequence and gene organization of A;Reference number: A/1000; MUID:98344137
A;Accession: H/1116
                                                                                                                    A;Cross-references: EMBL:293381; PIDN:CAB07607.1; GSPDB:GN00023;
A;Experimental source: clone F28G4
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A; Residues: 1-397 <K
                                                                                                                                                                          A; Residues: 1-450 <WIL>
                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T21515
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Best Local S
Matches 7
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Best Local S
Matches 7
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                             CESP:F28G4.4 osition: 5
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7; Conserv
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     52/3; 74/3; 104/3; 233/3; 293/3
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40;
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37;
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                                                                                                                                                  CESP: F28G4.4
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submitted to the EMBL Data Library, July 1991
A; Reference number: S40185
A; Accession: S40185
A; Molecule ****
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$12591
beta-1-adrenergic receptor - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change :
C; Accession: $12591; $40185; A35618
R; Shimomura, H.; Terada, A.
Nucleic Acids Res. 18, 4591, 1990
A; Title: Primary structure of the rat beta-1 adrenergic receptor
A; Title: Primary structure of the rat beta-1 adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33

S36794

beta-1-adrenergic receptor - mouse

c;Species: Mus musculus (house mouse)

c;Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999

C;Accession: S36794

C;Accession: S36794

D P - Chruscinski A.T: Kobilka, B.K.; Bernstein, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-26, 'A', 27-160, 'L', 162-174, 'R', 175-264, 'T', 266-464 <MAC>
A; Cross-references: GB: J05561; NID: 9203073; PIDN: AAA40792.1; PID: 9203074
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-25, 'A', 26-174, 'R', 175-464 <SH2>
A; Residues: 1-25, 'A', 26-174, 'R', 175-464 <SH2>
A; Cross-references: EMBL:D00634; NID:9220670;
R; Machida, C.A.; Bunzow, J.R.; Searles, R.P.;
J. Biol. Chem. 265, 12960-12965, 1990
A; Title: Molecular cloning and expression of tall and tall an
                                                                                                                                                           A;Cross-references: EMBL:L10084; NID:g293278; PIDN:AAA02929.1; PID:g293279 C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein
                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-466 < JAS>
                                                                                                                                                                                                                                                                                                                                                 A; Reference number: S36794; A; Accession: S36794
                                                                                                                                                                                                                                                                                                                                                                              R;Jasper, J.R.; Link, R.E.; Chruscinski, A.J.; Kobilka, B.K.; Bernstein, Biophim. Biophys. Acta 1178, 307-309, 1993
A;Title: Primary structure of the mouse beta (1)-adrenergic receptor gene. A;Reference number: S36794; MUID:93372116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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A;Cross-references: EMBL:D00634
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100.0%; Pred. No. 41;
tive 0; Mismatches
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Pred. No.
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R;Furtek, D.; Schiefelbein, J.W.; Johnston, F.; Nelson Jr., O.E. Plant Mol. Biol. 11, 473-481, 1988
A;Title: Sequence comparisons of three wild-type Bronze-1 alleles A;Reference number: S08324
A;Accession: S08325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Ralston, E.J.; English, J.J.; Dooner, H.K. Genetics 119, 185-197, 1988
A;Title: Sequence of three bronze alleles of maize A;Reference number: S01037; MUID:88284304
A;Accession: S01052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flavonol 3-0-glucosyltransferase (EC 2.4.1.91) (allele BzMcC2) - maize N;Alternate names: UDPglucose flavonoid glucosyl-transferase C;Species: Zea mays (maize) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: S08325
                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X07940; NID:g22204; PIDN:CAA30761.1; R;Furtek, D.; Schiefelbein, J.W.; Johnston, F.; Nelson Jr., O Plant Mol. Biol. 11, 473-481, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Zea mays (maize)
C;Date: 31-Dec-1990 #sequence_revision
C;Accession: S01052; S08324
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C;Superfamily: flavonol 03-glucosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase
A;Map position: 9
A;Introns: 175/1
C;Superfanily: flavonol 03-glucosyltransferase
C;Keywords: glycosyltransferase; hexosyltransfe
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-471 < FUR>
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A; Residues: 1-471 <FUR>
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                                                                                                                                                 A;Cross-references: EMBL:X13500; NID:g22364; PIDN:CAA31855.1; PID:g1030071
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3.0%;

Score Pred.

e 7; No.

DB 2;

Length 471;

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A;Gene: GDB:ADRB1; ADRB1R
A;Cross-references: GDB:19534; OMIM:109630
A;Map position: 10925-10925
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmentrane *status predicted <TM1>
F;S8-84/Domain: transmembrane *status predicted <TM2>
F;133-154/Domain: transmembrane *status predicted <TM3>
F;177-199/Domain: transmembrane *status predicted <TM4>
F;177-199/Domain: transmembrane *status predicted <TM5>
F;135-346/Domain: transmembrane *status predicted <TM5>
F;325-346/Domain: transmembrane *status predicted <TM5>
F;325-346/Domain: transmembrane *status predicted <TM5>
F;325-346/Domain: transmembrane *status predicted <TM5>
F;358-377/Domain: transmembrane *status predicted <TM5>
                                                                                                                                                                                                                                                                                                          153053

Deta I adrenergic receptor - rhesus macaque
C; Species: Macaca mulatta (rhesus macaque)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C; Accession: I53053
R; Searles, R.P.; Nipper, V.J.; Machida, C.A.
R; Searles, R.P.; Nipper, V.J.; Machida, C.A.
DNA Seq. 4, 231-241, 1994
A; Title: The rhesus macaque beta 1-adrenergic receptor gene: structure of tl
A; Reference number: I53053; MOID:95078456
A; Accession: I53053
                                                                                                                                                                                              A;Cross-references: EMBL:X75540; NI
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A39911
R;Frielle, T.; Collins, S.; Daniel, K.W.; Caron, M.G.; Lefkowitz, R.J.; Kobilka, Proc. Natl. Acad. Sci. U.S.A. 84, 7920-7924, 1987
A;Title: Cloning of the cDNA for the human beta-1-adrenergic receptor.
A;Reference number: A39911; MUID:88068509
A;Accession: A39911
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A; Residues: 1-480 < RES>
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C;Genetics:
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A; Residues: 1-477 <FRI>
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C;Date: 22-Jan-1993 #sequence_revision 18-Aug-1995 #text_change 22-Jun-1999
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C;Accession: JC7391
R;Endo, H.; Persson
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A; Residues: 1-508 < KUR>
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A;Molecule type: DNA
A;Residues: 1-485 <KUR>
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nes 7; Conserv
  H.; Persson, P.;
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, 9, e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, Y.P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.I.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: G98102...
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R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-556, 2001
                                                                                      N;Alternate names: DD4 protein
C;Species: Marsupenaeus japonicus
C;Date: 17-Nov-2000 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6) c;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 C;Accession: G98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: F95238
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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001
C;Accession: F95238
                   Biochem.
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                   Biophys.
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ilarity 100.0%;
Conservative
                     Res.
                                                                                                                                                               DD4 - prawn
                   Commun.
                                           Watanabe,
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100.0%; Pred. No.
                     276,
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Pred. No.
T.
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M.R.; Radune,
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Radune, D.; Holtzappl
                                                                                           18-Jul-2001
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, P.; McAhre
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hypothetical protein SSO3099 [imported] - Sulfolobus solfataricus C;Specias: Sulfolobus solfataricus C;Specias: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: D90493 R;She, Q; Singh, R.K.; Confalonieri, F; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Changon, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001 A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Molecular cloning of the crustacean DD4 cDNA encoding a A;Reference number: JC7391; MUID:20462952; PMID:11006119
A;Accession: JC7391
A;Molecule type: mRNA
A;Residues: I-542 <END>
C;Comment: This protein, acidic and proline-rich, is involved in C;Genetics:
                                                                                                                                                   A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.;
A;Title: Deciphering the biology of Mycobacterium
A;Reference number: A70500; MUID:98295987
A;Accession: E70546
A;Status: preliminary; nucleic acid sequence not s
                                                                                                                                                                                                                                                                                                                              RESULT 42
E70546
E70546
C;Species: Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: E70546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A99139
A;Accession: D90493
A;Status: pyreliminary
A;Molecule type: DNA
A;Residues: 1-548 <KUR>
A;Cross-references: GB:AE006641; NID:g13816517; PIDN:AAK43203.1;
                                         A; Experimental source: strain H37Rv C; Genetics: A; Gene: Rv0538
                                                                                               A; Cross-references: GB: 295558; GB: AL123456; NID: 93261781; PIDN: CAB08989.1; PID: e316975;
                                                                                                                   A; Molecule type: DNA
A; Residues: 1-548 <COL>
                                                                                                                                                                                                                                                R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Nature 393, 537-544, 1998
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C;Keywords: calcium binding
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100.0%; Pred. No. 49
Live 0; Mismatches
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tuberculosis fr
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from the complete genome
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                                                                                                                                                                                                                                                                                                          Gordon,
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T42100
conserved hypothetical protein PA4491 [imported] -
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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serine/threonine protein kinase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T36502
R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Raja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: pksc
C; Superfamily: Synechocystis sp.
C; Keywords: phosphotransferase;
                                                                                                                                                      A; Gene: pksC; SCOEDB: SCGD3.22
C; Superfamily: Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF094711; PIDN:AAC64406.1
C;Genetics:
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C; Species: Streptomyces coelicolor
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
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A; Residues: 1-556 <BAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, September 1998 A; Description: Cloning, nucleotide sequence and expression A; Reference number: Z22067
                                                                                                                                                                                                              A;Cross-references: EMBL:AL096822;
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-556 <SAU>
                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                    A; Reference number: Z21608
A; Accession: T36502
                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDB.
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                                 147 GTPAPAA 153
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GTPAPAA
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                                                                    Similarity 7; Conserved
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                                                                      Conservative
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353
                                                                                     3.0%;
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100.0%; Pred. No.
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                                                                                                                                                        sp.
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serine/threonine-specific protein kinase
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Pred.
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July 1999
                                                                    Mismatches
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                                                                                       DB 2;
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                                                                                                                                                          58K;
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                                                                    0;
                                                                                                      Length 556;
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                                                                                                                                                                                                                               GSPDB:GN00070;
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#text\_change 31-Dec-2000 Pseudomonas aeruginosa (strain

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-155,'T',157-267,'L',269-507,'E',509-599 <0ST>
A; Cross-references: GB:M23008; NID:g145679; PIDN:AAA23650.1;
R; Loudon, J.A.; Loughlin, R.E.
Gene 122, 17-25, 1992
A; Title: Mutagenesis and regulation of the cysJ promoter of I
A; Reference number: I41185; MUID:93083978
A; Accession: I41185
                                                                                                   C;Keywords: flavoprotein; NADP; oxidoreductase F;64-598/Domain: NADPH--ferrihemoprotein reductase homology F;66-205/Domain: flavodoxin homology <FLX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE000360; GB:U00096; NID:g2367157; PIDN:AAC75806.1; PID:g17 A;Experimental source: strain K-12, substrain MG1655 R;Ostrowski, J; Barber, M.J.; Rueger, D.C.; Miller, B.E.; Siegel, L.M.; Kredich, J. Biol. Chem. 264, 15796-15808, 1999 A;Title: Characterization of the flavoprotein moieties of NADPH-sulfite reductase ed from DNA sequence of cysJ, and comparison with NADPH-cytochrome P-450 reductase A;Reference number: A92735; MUID:89380164 A;Accession: B34231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A: Rose, .... 1453-1462, 1997 Science 277, 1453-1462, 1997 A:Title: The complete genome sequence of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sulfite reductase (NADPH) (EC 1.8.1.2) flavoprotein beta chain - Escherichi C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999 C;Accession: H65057; B34231; I41185 C;Accession: F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; L.Y., S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337
A;Accession: H83085
                                                                                                                                                               A;Gene: cysJ
C;Superfamily: sulfite
                                                                                                                                                                                                         C; Genetics
                                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                              A; Molecule type:
A; Residues: 1-29
                                                                                                                                                                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
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C; Superfamily: Escherichia
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A; Residues: 1-589 <STO>
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R; Stover, C.K.; Pham,
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    Similarity 7; Conser
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                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                   <RES>
es: GB:M65058; NID:g145677; PIDN:AAA23649.1;
  3.0%;
larity 100.0%;
Conservative
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                                                                                                                                                               reductase (NADPH); flavodoxin
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100.0%;
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L.L.; C
  Score 7; DB 1; Pred. No. 52; 0; Mismatches
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K.R.; Kas,
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                                                                                                                          <FEH>
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R;Perna, N.T.; Plunkett III, G.; liller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
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DNA Re: 8, 11-22, 2016
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91081
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C;Date: 18-Jul-2001 #sequence_revision
C;Accession: C91081
                                                                                                                                   C;Superfamily: sulfite reductase
C;Keywords: flavoprotein
                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: D85926
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A; Residues: 1-599 <STO>
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A; Residues: 1-599 <HAY>
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N.; Yasunaga, T.; Kuhara,
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Shiba, T.; Hattori,
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N;Alternate names: protein F9K21.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T47484
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
A;Accession: T47484
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R;Steane, D.A.; Scotland, R.W.; Mabberley, D.J.; Wagstaff, S.J.; Reeves, P.A.; Olmstead, submitted to the EMBL Data Library, July 1996
A;Description: Phylogenetic relationships of Clerodendrum s.l. (Lamiaceae) inferred from A;Reference number: Z17577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Clerodendrum incisum chloroplast C;Specias: chloroplast Clerodendrum incisum C;Decias: chloroplast Clerodendrum incisum C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 11-Jan-2000 C;Accession: T12712
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A;Note: F9K21.20
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases;
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Best Local Similarity
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A; Molecule type: DNA
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PRT1C_HUMAN STANDARD; PRT; 259 AA.

014798; 014755;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
10-MCT-2001 (Rel. 41, Last annotation update)
10-MCT-2001 (Rel. 41, Last annotation update)
11-OCT-2001 (Rel. 41, Last annotation update)
11-OCT-2001 (Rel. 40, Last sequence update)
11-OCT-2001 (Rel. 40, Last sequence update)
11-OCT-2001 (Rel. 40, Last sequence update)
11-OCT-2001 (Rel. 40, Created)
11-OCT-2001 (Rel. 40, 
   Sheridan J.P., Marsters S.A., Pitti R.M., Baldwin D., Ramakrishnan L., Gray C.L., B. Goddard A.D., Godowski P., Ashkenazi A.; "Control of TRAIL-induced apoptosis by a receptors.";
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MEDLINE-97461602; PubMed-9314565;
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Siol. Chem. 272:25417-25420(1997).
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MEDLINE=97467318; Pul
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Bell J.I., Screaton G.R.;
"Lymphocyte inhibitor of TRAIL (TNF-related apoptosis-inducing "Lymphocyte inhibitor protecting lymphocytes from the death
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N: Receptor for the cytotoxic ligand TRAIL.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., Cham., SEQUENCE FROM N.A., Cham., and real, TISSUE=Foreskin fibroblast, and real, TISSUE=98090091; PubMed=9430226; M.A., Dougall W.C., SF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T10D_HUMAN STANDARD Q9UBNS; Q9Y6Q4; 16-OCT-2001 (Rel. 40, C 16-OCT-2001 (Rel. 40, L 16-OCT-2001 (Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98044290; PubMed-9382840;
Marsters S.A., Sheridan J.P., Pit
Baldwin D., Yuan J., Gurney A., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor superfamily member 10D precursor (Decoy receptor 2) (DCR2) (TNF-related apoptosis-inducing ligand receptor 4)
(TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death
                                                                                                             FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fetal lung;
MEDLINE=98044290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                          TRAIL signalling.";
                                                                                                                                                                    Pan G., Ni J., Yu G.-L., Wei
"TRUNDD, a new member of the
                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
MEDLINE=98196860; P
                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                        TRAIL-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashkenazi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNFRSF10D OR DCR2 OR TRAILR4 OR TRUNDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
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hes 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              novel
  apoptosis
are contra
                                                   FUNCTION: Receptor for truncated death domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel receptor TRAIL-R4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTSWDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor for Apo2L/TRAIL ol. 7:1003-1006(1997).
                                                                                                                                                                                                                                                                                                         1iated apoptosis,
7:813-820(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Human)
                            but protects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΑA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                           PubMed=9537512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
27395
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                                                                                                                                                                                                                                                  AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                   yet
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                         the cytotoxic ligand TRAIL. Contains and hence is not capable of inducing against TRAIL-mediated apoptosis. Rep
                                                                                                                                                                    i Y.-F.,
e TRAIL r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                             induces
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E -> V (IN REF. 5)
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                      retains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pitti R.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 233;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FE3BF7FCEEAE50B8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-TERMINUS, AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contains
  ţ
                                                                                                                                                                    receptor
                                                                                                                                          Dixit V.M.; receptor family that antagonizes
                                                                                                                                                                                                                                                                                                                                NF-kappaB and ps an incomplete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386
  its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND VARIANTS S-35 AND heral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.D., Godowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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1.2e-238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Waugh J.Y., Smith C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                   protects ag
e death doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skubatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        death domain.";
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the NF-
                                                                                                                                                                                                                                                                                                                                   against
lomain.";
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В
               QY
                                                                                   Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                          Receptor; Apopolymorphism. SIGNAL
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DISULFID
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF029761; AAD03477.1; -.
EMBL; AF021233; AAC32765.1; -.
EMBL; AF021233; AAC32766.1; -.
EMBL; AF023849; AAC32053.1; -.
HSSP; P19438; 1NCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>:</del> :
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00020; TNFR_c6; SMART; SM00208; TNFR; 2
                                                                                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                   SEQUENCE
                                                                                                      VARIANT
                                                                                                                        VARIANT
                                                                                                                                   CARBOHYL
                                                                                                                                            CARBOHYD
                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50050;
                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
93
                 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kappaB pathway (According to ref.1 it cannot but according ref.2 it can induce the NF-KappaB pathway)
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Widely expressed, in particular in fet kidney, lung & liver and in adult testis and liver. Also es in peripheral blood leukocytes, colon and small intestine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate, thymus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through 
een the Swiss Institute of Bioinformatics and the El
                 TGACNPCTEGVDYT
                                                                                                                                                                                                                                                                                                                                                                                    603614;
                                  ch 6.0%;
l Similarity 100.0%;
l4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               PS00652;
                                                                                                                                                                                                                                                                                                                                                                IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                            Apoptosis; Glycoprotein;
                                                                                   386
                                                                                                                        212
233
233
140
340
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226
246
246
1181
1181
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1158
1162
1162
1187
                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                              TNFR_NGFR_1;
                                                                                                                        386
                 50
                                                                                   41823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spleen, pancreas, kidney, lung, placenta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TNFR-CYS REPEATS.
1 DEATH DOMAIN (TRUNCATED).
                                                                                   ME.
                                                                                POTENTIAL.

N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
P-> S (IN TRAIL-R4-B).

/FTId=VAR 011417.

S-> L (IN TRAIL-R4-B).

/FTId=VAR 011418.

W; 77A93577CAAF2632 CRC64
                                  Score 14; DB; Pred. No. 4.8
                                    0
                                                                                                                                                                                                                                                                    TUMOR NECROSIS I SUPERFAMILY MEME EXTRACELLULAR (FPOTENTIAL.
                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                             POLY-VAL.
                                                                                                                                                                                                                                DEATH
                                                                                                                                                                                                                                          TNFR-CYS
                                                                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                            Transmembrane; Repeat; Signal;
                                                                                                                                                                                                                                 (TRUNCATED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions ing as its content is in
                                           DB 1; 1
4.8e-07
                                                                                                                                                                                                                                                                                        MEMBER
                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                     Length 386;
                                                                                   CRC64;
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                                                                                                                                 (POTENTIAL)
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                                  Gaps
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T10B\_HUMAN STANDARD; PRT; 440 AA.

ID T10B\_HUMAN STANDARD; PRT; 440 AA.

AC 014763; 015531; 015508; 015517; 014720; Q9BVE0;

DT 16-0CT-2001 (Rel. 40, Created)

DT 16-0CT-2001 (Rel. 40, Last sequence update)

Created) Last sequence update)

RESULT

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SEQUENCE FROM N.A. (SHOKE LUCL.)
MEDLINE-97390509; PubMed-9242611;
Sheridan J.P., Marsters S.A., Pitti R.M.,
Sheridan J.P., Ramakrishnan L., Gray C.L., B.
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Science
[6]
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MEDLINE-97390508; PubMed-9242610;
MEDLINE-97390508; Properties of the second secon
                                                                                                                                                                                                                 MEDLINE=98090092; PubMed=Chaudhary P.M., Eby M., J
"Death receptor 5, a new
FADD-dependent apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cohen G.M., Alnemri E.S.; "Identification and molecular cloning
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[5]
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"Characterization of two receptors
FEBS Lett. 416:329-334(1997).
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Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel
Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.
"KILLER/DR5 is a DNA damage-inducible p53-regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97467719; PubMed=9326928; Wu G.S., Burns T.F., McDonald E.R.
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"TRAIL-R2: a novel apoptosis-mediating receptor EMBO J. 16:5386-5397(1997).
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Mammalia; Eutheria; Primates;
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receptor-2) (TRAIL-R2).
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NF·related apoptosis·inducing ligand receptor 2) (TRAIL
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PubMed=9373179;
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                                                                                                                                                                                                                 M., Jasmin A., Bookwalter A., Murray J., a new member of the TNFR family, and DR4 tosis and activate the NF-kappaB pathway.
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"Triggering cell death: the crystal structure of Apo2L/TRAIL in complex with death receptor 5.";
Mol. Cell 4:563-571(1999).
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                                                                                                                                                                                                                                                                                             Jones E.Y., Screaton G.R.;
"Structure of the TRAIL-DR5 complex reveals mechanisms conferring specificity in apoptotic initiation.";
Nat. Struct. Biol. 6:1048-1053(1999).
                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) PubMed=10542098;
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en the Swiss Institute of Bioinformatics
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                                           and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
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T., Gilbert T., Gross J.,
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Okabe S., Saito K.,
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EMBL;

AF018657; AF018658; AF016266;

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AC Q9XIM6
DT 16-OCT
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DT Elagel
GN FLGH O
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Best Loc
Matches
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Pfam; PF00020; TNFR_C6; 2.

SMART; SM00005; DEATH; 1.

SMART; SM00208; TNFR; 2.

PROSITE; PS50017; DEATH_DOMAIN; 1.

PROSITE; PS00652; TNFR_NGFR_1; 2.

PROSITE; PS00655; TNFR_NGFR_1; 2.

PROSITE; PS00655; TNFR_NGFR_1; 2.

Receptor; Apoptosis; Transmembrane; Ralternative splicing; 3D-structure.
16-OCT-2001 (Rel. 40, Crea

16-OCT-2001 (Rel. 40, Last

16-OCT-2001 (Rel. 40, Last

16-OCT-2001 (Rel. 40, Last

Flagellar L-ring protein p

FLGH OR TM1540.

Thermotoga maritima.

Bacteria; Thermotogales; T.

NCBI_TaxID-2336;

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EMBL; AB015
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InterPro; IPR001368; TNFR_c6
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AF020501
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AF016268
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AAH01281
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BAA33723
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AAB67109.
AAB71412.
AAC01565.
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EXTRACELLULAR (POTENTIAL).
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RX MEDLINE-99287316; PubMed-10360571;
RX MEDLINE-99287316; PubMed-10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria fro
genome sequence of Thermotoga maritima.";
RI Nature 399:323-339(1999).
CC -i- FUNCTION: ASSEMBLES AROUND THE ROD TO FORM THE L-RING AND PROBAI
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16-CCT-2001 (Rel. 4
16-CCT-2001 (Rel. 4
16-CCT-2001 (Rel. 4
Hypothetical 20.2 k
RV1911C OR MT1962 (
MEDLINE-98295987; PubMed-9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.
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007722;
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CHAIN
SEQUENCE
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                                                                                                                                                                                            SEQUENCE FROM STRAIN=H37RV;
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PRINTS: PR01008; FLGLRINGFLGH.
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Bacteria; Firmicutes; Acti
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NCBI_TaxID=1773;
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SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED SIMILARITY: BELONGS TO THE FLGH FAMILY.
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SUBUNIT: THE BASAL
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|VLLIVF
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S; PRO1008; FLGLRINGE LOGIC
La; Outer membrane; Signal; C
12 25 POTENT
12 19 FLAGE!
12 28 MW; D2A
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Similarity 100.0%;
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                . 39, Created)
. 40, Last sequence upon 40, Last annotation 12 kDa protein Rv191IC. 2 OR MTCY180.07.
                                                                                                                                                                                                                                                                                              Corynebacterineae;
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Pred. No. 6.4
0; Mismatches
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FLAGELLAR L-RING PF
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Best Local
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the Euro
use by
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Nature 393:537-544(1998).

1200ENCE FPOT:
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Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                             Sastre
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Artemiidae; Artemia
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                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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b; Pred. No. 6.6
0; Mismatches
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Bacteria; Firmicutes; Actinobacte.
Actinomycetales; Streptomycineae;
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                                                                                                                                                                                                                                         EMBL; M73758; PIR; S27708;
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SIMILARITY: BELONGS
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DRRB MAY ACT JOINTLY TO CC
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6; 1;
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TRANSMEM 175 195
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TRANSMEM 273 293
TRANSMEM 329 349
SEQUENCE 374 AA; 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDB1_SCHPO STANDARD; PRT; 374 AA. 010354; Q9URX5; 01-OCT-1996 (Rel. 34, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical 42.3 kDa protein C22E12.01 in chspacc2E12.01 OR SPACC2E12.01 or SPACC2E12.01
LA_DROME STANDARD;
P40796; Q24375; Q9VIN2;
O1-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Devlin K., Churcher C.M., Submitted (MAR-1996) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saunders D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 MTTSPGT 178
                                                                                                                                                         222 IIVLIVL 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh smitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation service and the EMBL outstation services and the service on its suropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                         Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
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Pred. No.
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                                                                                                                                                                                         Mismatches
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11;
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                                                                                                                                                                                                                        Length 374
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   SUBCELLULAR LOCATION: Nuclear (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol.
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Hallew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Beasu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Glerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies C., Dunn P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gana P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibegvam C.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattel B., McIntosh T.C., Mcroit J., Parl B., Ketchum K.A.,
RA McInulla B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA McInulla B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA McInulla B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
RA McInulla B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
RA McInulla B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
RA McInulla B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
RA McInulla B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
RA McInulla B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A.,
RA McInulla B.E., Kodira C.D., Fang K., Lin X., V., Moshrefi A.,
RA McInulla B.E., Kodira C.D., Fang K., Lin X., V., Moshrefi A.,
RA McInulla B.E., Kodira C.D., Fang K., Nusskern D.R., Pacleb J.M.,
Ra McInulla B.C., Stapheton M., Stupski M.P., Smith T.,
Ra McInulla B.C., Scapheton M., Stupski M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerevisiae: a yeast
growth.";
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STRAIN=CANTON-S; TISSUE=Ovary;
MEDLINE=94309632; Pubmed=8035794;
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16-OCT-2001 (Rel. 40, Last annotation update)
La protein homolog (La ribonucleoprotein) (La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
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FUNCTION: MAY BE INVOLVED IN TRANSCRIPTION TERMINATION POLYMERASE III. BINDS RNA AND DNA. BINDS TO PRECURSORS POLYMERASE III TRANSCRIPTS. MAY PLAY A SPECIALIZED ROLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoantigen."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophilidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homolog of the La
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Endopterygota; Diptera; Brachyce
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P50134;
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01-OCT-1996 (Rel. 34, 1
01-NOV-1997 (Rel. 35, 1
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DOMAIN 149 234 RI
CONFLICT 169 169 A
CONFLICT 182 183 KI
CONFLICT 283 283 A
CONFLICT 329 329 K
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                                                                            Datura stramonium (Jimsonweed) (Common thornapple). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Datura.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
0rnithine decarboxylase (EC 4.1.1.17) (ODC).
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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InterPro; IPR002344; Lupus_La.
InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 1.
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                                          OF POLYAMINE BIOSYNTHESIS SIMILARITY: BELONGS TO FA
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SM00360; RRM; 1.
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AND ADULT DEVELOPMENT. EXPRESSION THROUGHOUT THE EMBRYO IS
ED BY A RESTRICTED PATTERN OF MESODERMAL EXPRESSION THAT IS
CONFINED TO THE VISCERAL MESODERM, GONADS, GUT, AND SALIVARY
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KH -> NS (IN REF. 1).

A -> R (IN REF. 1).

K -> N (IN REF. 1).

K -> N (IN REF. 1).
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0; Mismatches
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RNA-BINDING (RRM)
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RESULT 11
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Jasper J.R., Link R.E., Chruscinski A.J., Kobilka B.K., Bern Primary structure of the mouse beta 1-adrenergic receptor g Biochim. Biophys. Acta 1178:307-309(1993).

C.-!- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOL INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTIPROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPH C PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPH APPROXIMATIVELY EQUAL AFFINITY.

C.-!- SUBCELIULAR LOCATION: Integral membrane protein.

C.-!- SUBCELIULAR LOCATION BY BETA-ADRENERGIC RECEPTOR KINASE.

C.-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTOR SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTOR MEDIAMENTAL PROCESSES AND ADDRENERGIC RECEPTOR KINASE.
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Best Local
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EMBL; L10084; AAA0292
PIR; S36794; S36794.
HSSP; P07700; 1DEP.
GCRDb; GCR_0578; -.
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01-FEB-1994 (Rel. 3
01-NOV-1995 (Rel. 3
Beta-1 adrenergic r
ADRB1 OR ADRB1R.
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or send a
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ACT_SITE
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                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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HSSP; P00860; 7ODC.
InterPro; IPR000183; Orn_DAP_Arg_decarbxylse.
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STRAIN=129/SV;
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PROSITE; PS00878; ODR_DC_2_1; 1.
PROSITE; PS00879; ODR_DC_2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02784; Orn_Arg_deC_N; 1.
Pfam; PF00278; Orn_DAP_Arg_deC; 1.
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Similarity 100.0%; Pred. No.
7; Conservative 0; Mismatc
                                                                            an email to license@isb-sib.ch).
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431 AA;
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                                             AAA02929.1;
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28, Last sequence update)
32, Last annotation update)
receptor.
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                                                                                                           Usage
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HROUGH THE ACTION OF G
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P18090;
01-NOV-1990 (Rel. 16, 0
01-NOV-1990 (Rel. 16, 1
01-NOV-1995 (Rel. 32, 1
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Multigene
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PROSITE; PS00237; G_PROTEIN_RI
PROSITE; PS50262; G_PROTEIN_RI
            "Primary structure of the rat beta-1 adrenergic receptor gene.";
Nucleic Acids Res. 18:4591-4591(1990).
-IFUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE APPROXIMATIVELY EQUAL AFFINITY.
                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=90330633; Machida C.A., Bunz
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                                                                                    Shimomura H., Terada A.;
                                                                                                              SEQUENCE FROM
                                                                                                                                                  receptor
                                                                                                                                                          Machida C.A., Bunzow J.R., Searles R.P., v
Neve K.A., Teal P., Nipper V., Civelli O.,
"Molecular cloning and expression of the r
                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                 MEDLINE=90356399; PubMed=2167473;
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nilarity 100.0%;
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  LOCATION:
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G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_RECEP_F1_2; 1.
I receptor; Transmembrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                    PubMed=1695899;
                                                                                                                                                                                                                                                                                                    receptor.
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CYTOPLASMIC (POTENTIAL).

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PHOSPHORYLATION (BY CAPK)
PHOSPHORYLATION (BY CAPK)
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                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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 membrane protein
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Eukaryota;
Mammalia; E
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Multigene
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EMBL; D00634; BAA00527.1; -.
PIR; A36618; A36618.
PIR; S12591; S12591.
HSSP; P07700; IDEP.
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PRINTS; PR00237; GPROTEIN_RE
PROSITE; PS00237; G_PROTEIN_RE
PROSITE; PS50262; G_PROTEIN_RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCRDb; GCR_0126; -.
GCRDb; GCR_0127; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                     LIVLLIV
                                                                                                                                                                           Similarity 7; Conserv
Ea (Pig).
a; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          family;
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G_PROTEIN_RECEP_F1_2; 1.
                                               36,
37,
38,
                                      receptor
Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                    3.0%;
100.0%;
                                              Last sequence up
                                                                  Created)
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CYTOPLASMIC (POTENTAL)
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PHOSPHORYLATION (BY CAPK)
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                                               on update)
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Multigene
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

INUCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G
PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
APPROXIMATIVELY EQUAL AFFINITY (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adrenergic receptor gene.";
J. Anim. Sci. 76:1720-1721(1998).
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Cao H., Bidwell C.A., Williams S.K.,
"Nucleotide sequence of the coding radraperate recentry dene".
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                             Similarity 7; Conserv
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G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitate.
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L -> V (IN REF. 2).
CWL -> WWV (IN REF. 2).
R -> A (IN REF. 2).
T -> S (IN REF. 2).
AS -> SF (IN REF. 2).
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Pred. No.
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CYTOPLASMIC (POTENTIAL).
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4 (POTENTIAL)
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16-OCT-2001 (Rel. 40, 0
16-OCT-2001 (Rel. 40, 1
16-OCT-2001 (Rel. 40, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement 'care' or send an email to ''are'.
                                                                                                                                                                                                InterPro; IPR001368; TNFR_c
pfam; pF00531; death; 1.
pfam; pF00020; TNFR_c6; 2.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis in a caspase-dependent manner. Can trigger the nuclear factor kappaB-pathway and can bind the cytoplasmic adapter molecule FADD/MORTI which engages initiator caspases such as caspase 8 leading to subsequent activation of effector caspases that execute apoptotic death of the cell.

SUBGURIT: Can interact with TRADD and RIP.

SUBCLLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Widely expressed. High levels are found in spleen, peripheral blood leukocytes, small intestine and thymus, but also in K562 erythroleukemia cells, MCF7 breast carcinoma cells and activated T-cells.

SIMILARITY: CONTAINS 2 TNET-CYS REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan G., O'Rourke K., Chinnalyan A.M., Genez R., Dixit V.M.;
"The receptor for the cytotoxic ligand TRAIL.";
Science 276:111-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor necrosis factor receptor superfamily member 10A precursor (Death receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL receptor-1) (TRAIL-R1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood I "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway."; Immunity 7:821-830(1997).
                                                                                                                                                                                                                                                                                                                                                                               EMBL; U90875;
HSSP; P19438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                             InterPro; IPR000488; Death
                                                                                                                                                                                                                                                                                                                                                          MIM; 603611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                          PS50017;
PS00652;
PS50050;
                                                                                                Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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1EXT.
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                                                                                                                          DEATH_DOMAIN; 1.
TNFR_NGFR_1; 2.
TNFR_NGFR_2; 2.
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K., Chinnaiyan A.M.,
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Last annotation updat
SUPERFAMILY MEMBER EXTRACELLULAR (POTE
                                                 TUMOR NECROSIS FACTOR RECEPTOR
                                                                              POTENTIAL.
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Matches 7
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01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Flavonol 3-0-glucosyltransferase (EC 2.4.1.91) (UDP-glucose
3-0-glucosyltransferase) (Bronze-1) (BZ-MCC allele).
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DOMAIN
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MEDLLINE=88284304; PubMed=3396861;

Raiston E.J., English J.J., Dooner H.

"Sequence of three bronze alleles of
genetic fine structure.";

Genetics 119:185-197(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
Panicoideae; Andropogoneae; Zea.
EMBL; X13500; CAA31855.1;
EMBL; X07940; CAA30761.1;
PIR; S01052; S01052.
PIR; S08324; S08324.
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Furtek D., Schiefelbein
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                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR UGT71A1.
                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                             3-0-D-glucoside.
PATHWAY: Anthocyanin biosynthesis
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an email to license@isb-sib.ch).
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01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (UDP-glucose flavonoid 3-O-glucosyltransferase) (Bronze-1) (BZ-MC2 allele).
BZ1 OR UGT71A1.
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InterPro; IPRO02213; UDPGT.
pfam; pF002201; UDPGT; 2.
PROSITE; PS00375; UDPGT; 1.
Transference
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Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Charryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
                                                                                                                                                                                                                                                       InterPro; IPR002213; UDPGT
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PROSITE; PS00375; UDPGT; 1.
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SEQUENCE 471 AA; 48769 MW; 6234FD59219AF534 CRC64;
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InterPro; IPR00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Furtek D., Schiefelbein J.W., Johnston F., Nelson O.E. "Sequence comparisons of 3 wild-type bronze-1 alleles plant Mol. Biol. 11:473-48(1988).
-i- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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Panicoideae; Andropogoneae; Zea.
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SEQUENCE 471 AA; 48621 MW; 81B897410A361299 CRC64;
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MaizeDB; 13885; -.
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MEDLINE-97364078; PubMed-9220370;
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- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF GPROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH
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SUBCELLULAR LOCATION: Integral membrane protein.
PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS
PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE
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            Ŗ,
Y: Phosphorylation; Lipoprotein; Palmitate.

59 EXTRACELLULAR (POTENTIAL).

96 CYTOPLASMIC (POTENTIAL).

120 2 (POTENTIAL).

131 EXTRACELLULAR (POTENTIAL).

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G_PROTEIN_RECEP_F1_2; 1.
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                                    PHOSPHORYLATION (BY CAPK) (POTENTIAL) PALMITATE (BY SIMILARITY).
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                                                                                                                                                                                                           Borjesson M., Magnusson Y., Hjalmarson A., Andersson B.;

"A novel polymorphism in the gene coding for the beta(1)-adrenergic receptor associated with survival in patients with heart failure.";

EUT. Heart J. 21:1853-1858(2000).

-i- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF APROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATIVELY EQUAL AFFINITY.

APPROXIMATIVELY EQUAL AFFINITY.

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY 1 PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.

-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                EMBL;
EMBL;
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PIR; /
                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                   This
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"A gain-of-function polymorphism in a
human betal-adrenergic receptor.";
J. Biol. Chem. 274:12670-12674(1999).
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P08588; Q9UKG8; Q9UKG7;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Beta-1 adrenergic receptor.
ADRB1 OR ADRB1R OR BIAR.
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Blar_HUMAN
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"Racial differences in the frequencies of cardiac beta(1)-adrenergic 
receptor polymorphisms: analysis of c145A>G and c1165G>C."; 
Hum. Mutat. 14:271-271(1999).
                                                                                                                                                                     between
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Kobilka B.K.
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                ; J03019; AAA51667.1; -.; AF169006; AAD53696.1; -; AF169007; AAD53697.1; -A39911; A39911.
                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the cDNA for the human beta 1-adrenergic receptor.", Acad. Sci. U.S.A. 84:7920-7924(1987).
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ns S., Daniel K.W.,
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100.0%; Pr
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; pF00001; 7tm_1; 1.
PRINTS; pR00237; GPCRRHODOPSN.
PRINTS; pR00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
   Searles R.P., Nipper V.J., Machida C.A.;
"The rhesus macaque beta 1-adrenergic receptor gene: structure of gene and comparison of the flanking sequences with the rat beta 1 adrenergic receptor gene.";
DNA Seq. 4:231-241(1994).
-i- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE FUNCTION: BETA-ADRENERGIC RECEPTORS THROUGH THE ACTION OF ADENYLATE CYCLASE THROUGH THE ACTION OF ADENYLATE CYCLASE THROUGH THE CYCLASE THROUGH THROUGH THROUGH THROUGH THROU
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%; Pred. No. 14;
0; Mismatches
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CYTOPLASMIC (FOTENTIAL).
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3 (POTENTIAL)
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2 (POTENTIAL)
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5 (POTENTIAL).
                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Cercopithecidae;
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1D15E6390B5364B8 CRC64;
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PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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Best Local
SEQUENCE FROM N.A., AND PARLIAL STRAIN-STOCK 51;
MEDLINE-95024055; PubMed-7937900;
Subramanian S.V., Wyroba E., Andersen Subramanian G.V., Wyroba E., Andersen Subramanian S.V., Wyroba E., Andersen S.V., Wyroba E., W
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PARE_PARTE
P47244;
01-FEB-1996
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                                                                                                                                                                                                                                                                                        Paramecium tetraurelia
Eukaryota; Alveolata;
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Pfam; PF00001; 7tm_1; 1.
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G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_RECEP_F1_2; 1.
I_receptor; Transmembrane; Glycoprotein;
Palmitate.
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PHOSPHORYLATION (BY CAPK) (POTENTIAL).
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                                                               Satir B.H.;
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RESULT 22
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Best Local
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HSSP; P00949; 3PMG.
Interpro; IPR001485; PGM_PMM.
Pfam; PF00408; PGM_PMM; 1.
Pfam; PF02878; PGM_PMM_I; 1.
Pfam; PF02879; PGM_PMM_II; 1.
Pfam; PF02880; PGM_PMM_III; 1.
                                                                                                                                                    P38038; P14782;
01-OCT-1994 (Rel.
01-OCT-1996 (Rel.
01-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                  USCROWSKI J.,
Kredich N.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS
Satir B.H.
                                                                                                        Escherichia coli.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Carbohydrate cycling in signal transduction: para phosphoglycoprotein and possible Ca(2+)-dependent
"Characterization of the flavoprotein reductase from Salmonella typhimurium
                                           MEDLINE=89380164;
                                                                  SEQUENCE
                                                                                     NCBI_TaxID=562;
                                                                                                 Escherichia
                                                                                                                               CYSJ OR B2764.
                                                                                                                                                                                                           CYSJ_ECOLI
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation. ACT_SITE 138
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34, Last sequence update)
40, Last annotation updat
[NADPH] flavoprotein alph
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bred. No. 17;
Mismatches
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  Escherichia
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lent transducer molecule
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          of NADPH-sulfite
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EcoGene; EG10191; cysJ.

EcoGene; EG10191; cysJ.

Interpro; IPR003097; FAD_binding.

Interpro; IPR001094; Flavdxn-like.

Interpro; IPR001226; Flavodoxin.

Interpro; IPR001276; Flavodoxin.

Interpro; IPR001433; Oxidored_FAD.

Pfam; PF00657; FAD_binding; 1.

Pfam; PF00258; flavodoxin; 1.

Pfam; PF00175; NAD_binding; 1.

PRINTS; PR00369; FIAVODOXIN.

PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M23008; AAA23550.1; .
EMBL; U29579; AAA69274.1; -.
EMBL; AE000360; AAC75806.1; -.
EMBL; B34231; B34231.
NP_BIND
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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between
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J. Biol. Chem. 264:15726-15737(1989).

-i-FUNCTION: THIS ENZYME CARLAYZES THE SELECTRON REDUCTION OF SULFITE TO SULFIDE. THIS IS ONE OF SEVERAL ACTIVITIES REQUIRED FOR THE BIOSYNTHESIS OF L-CYSTEINE FROM SULFATE. THE FLAVO-PROTEIN COMPONENT CATALYZES THE ELECTRON FLOW FROM NADPH ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                Cysteine INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                       NP_BIND
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                                                                                                                                   NP_BIND
                                                                                                                                                                                                                                         Oxidoreductase; Flavoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97426617; PubMed-9278503;
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SUBUNIT: ALPHA(8)-BETA(4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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CATALYTIC ACTIVITY: H(2)S + 3 NADP(+) + 3 H(2)O =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: ALPHA(8)-BETA(4). THE ALPHA COMPONENT IS A FLAVOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence
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J.-Y., Rueger D.C.,
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    X.
                      NADP
T ->
L ->
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FMN (PYRIMIDINE PART) (
FAD (PYROPHOSPHATE MOIE
(BY SIMILARITY).
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ADP (PYRIMIDINE MOIETY) (BY SIMILARITY)

> S (IN REF. 2).

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OB6EEE0E2E70F13E CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 117.4 kDa protein C3H1.02C in ch
SPAC3H1.02C.
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                                                                                                                                     Q9X7F0;
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
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Hypothetical protein.
SEQUENCE 1036 AA; 117421 M
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MEDLINE=21128732;
Cole S.T., Eiglme
                                                           Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; MCBI_TaxID=1769;
                                                                                                              DNA polymerase III alpha son DNAE OR ML1207 OR MLCB458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                         STRAIN-TN
                                      SEQUENCE
                                                                                                  Mycobacterium leprae.
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PubMed=11234002;
ier K., Parkhill
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100.0%; Pred. No. 17
tive 0; Mismatches
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B458.21.
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 Thomson
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SEQUENCE FROSTRAIN-M145;
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16-OCT-2001 (Rel. 40,
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16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                           _STRCO
                                                                           Streptomyces coelicolor Bacteria; Firmicutes; Ac
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DNAE OR SC4G6.33C
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                                            Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-i- FUNCTION: DNA POLYMERASE III IS A COMPLEX.
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InterPro; IPRO03141; PHP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leproma; ML1207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THE CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE COD DIMERIZATION TO FORM THE POLITI' COMPLEX. POLITI'A ASSOCIATES THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PAND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPIASMIC (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPIASMIC (BY SIMILARITY). BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: DNA POLYMERÁSE III IS A COMPLEX, MULTICHAIN ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYMPHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY. THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY). CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphospha
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PF02231; PHP_N; 1.
PF01336; tRNA_anti; 1.
; SM00481; POLIIIAC; 1.
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AL583921; CAC31588.1;
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1177 AA;
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                                                                                                                           III alpha
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                                                              Streptomycineae;
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Last annotation updat
                                                                           Actinobacteria; Actinobacteridae;
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                                                           Streptomycetaceae; Streptomyces
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DP3A_MYCTU
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Best Local S
Matches 7
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EMBL; AL096884; CAB51456.1; -.
InterPro; IPR004013; PHP_C.
InterPro; IPR003141; PHP_N.
InterPro; IPR002309; trNA-synt_2.
Pfam; PF02811; PHP_C; 1.
Pfam; PF02811; PHP_C; 1.
Pfam; PF0281; PHP_N; 1.
Pfam; PF01336; trNA_ant1; 1.
SMART; SM00481; PCLIIIAC; 1.
                                                                                                                           DP3A_MYCTU STANDARD; PRT; 1184 AA. Q10779; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) DNA polymerase III alpha subunit (EC 2.7.7.7) DNAE OR DNAE1 OR RV1547 OR MT1598 OR MTCY48.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; DNA-directed DNA polymerase; DNA replication VARIANT 802 802 E -> K (IN MUTANT TS-38). SEQUENCE 1179 AA; 130795 MW; 7E4B58675B634CD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
Bacteria; Firmicutes; Actir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Smith C.P.;
"A 'Gram-negative-type'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
                                                    Actinomycetales;
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                                                    Corynebacterineae;
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Pred. No. 32;
0; Mismatches
                                                    Mycobacteriaceae;
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32;
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COLe S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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InterPro; IPRO03141; PHP_N.
InterPro; IPRO02309; tRNA-s;
Pfam; PF02811; PHP_C; 1.
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158
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                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - EDUTOPEAN BIOINFORMATICS Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
CPSGEVQ
                           CPSGEVQ
                                                                                                                                                                                PF02231; PHP_N; 1.
PF01336; tRNA_ant1; 1.
SM00481; POLITIAC; 1.
                                                                                                                                                                                                                                                                                                      MT1598;
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                                                         Similarity 7; Conserv
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                                                           Conservative
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                                                                      3.0%;
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                                                                                                                                    129322
                                                                                                                                                                 DNA polymerase; DNA replication;
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                                                           0;
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Pred. No.
                                                           Mismatches
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32;
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Mikula A.,
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                                                                                                                                       30-MAY-2000
30-MAY-2000
16-OCT-2001
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MEDLINE-96270742.
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Q9Z0Y8;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eur. J. Biochem. 236:904-910(1996).
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                                                                                                        Voltage-dependent
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Bacillus/Staphylococcus group; Staphylococcus.
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IN NEUROSCI. 19:1912-1921(1999).

11. FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-11 GIVES RISE TO T-TYPE CALCIUM CURRENTS. T-TYPE CALCIUM CHANNELS BELOMG TO THE "LOW-OULTAGE ACTIVATED (LVA)" GROUP AND ARE STRONGLY BLOCKED BY NICKEL AND MIBEFRADIL. A PARTICULARITY OF THIS TYPE OF CHANNELS IS AN OPENING AT QUITE NEGATIVE POTENTIALS, AND A VOLTAGE-DEPENDENT INACTIVATION. T-TYPE CHANNELS SERVE PACEMAKING FUNCTIONS IN BOTH CENTRAL NEURONS AND CARDIAC NODAL CELLS AND SUPPORT CALCIUM SIGNALING IN SECROTORY CELLS AND VASCULAR SMOOTH MUSCLE. THEY MAY ALSO BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING AS WELL AS IN CELL GROWTH PROCESSES. GATES IN VOLTAGE RANGES SIMILAR TO, BUT HIGHER THAN ALPHA 1G OR ALPHA 1H.

1. SUBCELLULAR LOCATION: Integral membrane protein.

1. TISSUE SPECIFICITY: BRAIN.

1. DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE PROBABLY REPRESSINT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

1. POTM: IN RESPONSE TO RAISING OF INTRACELLULAR CALCIUM, THE T-TYPE CHANNELS ARE ACTIVATED BY CAM-KINASE II (BY SIMILARITY).

1. SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.
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eerPro; IPR002077; Ca_channel.
eerPro; IPR002101; Cat_channel_TrpL.
eerPro; IPR002111; Cat_channel_TrpL.
eerPro; IPR001636; Cation_chan_non_lig.
eerPro; IPR001682; Channel_pore_Ca_Na.
mm; PF00520; ion_trans; 4.
NTS; PR00167; CACHANNEL.
id channel; Transmembrane; Ion transport
ctum_channel; Glycoprotein; Repeat; Mult
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CYTOPLASMIC (POTENTIAL).

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                                                Last sequence update)
Last annotation update)
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S2 OF REPEAT III (POTENTIAL).

S3 OF REPEAT III (POTENTIAL).

S3 OF REPEAT III (POTENTIAL).

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S4 OF REPEAT III (POTENTIAL).

S5 OF REPEAT III (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S6 OF REPEAT III (POTENTIAL).

S6 OF REPEAT III (POTENTIAL).

S7 OF REPEAT IV (POTENTIAL).

S1 OF REPEAT IV (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).

S5 OF REPEAT IV (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

S6 OF REPEAT IV (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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S4 OF REPEAT II (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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S5 OF REPEAT II (POTENTIAL).
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(BY SIMILARITY).
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$6 OF REPEAT II (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

$1 OF REPEAT III (POTENTIAL)
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WEDLINE-Small intestine mucosa;

WEDLINE-89066802; PubMed-3143729;

A Naim H.Y., Sterchi E.E., Lentze M.J.;

"Structure, biosynthesis, and glycosylation of maltase-glucoamylase.";

J. Biol. Chem. 263:19709-107777777
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the Euro
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  DOMAIN
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InterPro; IPR000519; P_trefoil.
Pfam; PF01055; Glyco_hydro_31; 2.
Pfam; PF00088; trefoil; 2.
SMART; SM00018; P; 2.
                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
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"Tyrosine sulfation,
enzymes in the small
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                                                                                                            Multifunctional enzyme; Transmemora
                                                                                                                                                                                                                                                                                                 EMBL; AF016833; AAC39568.1; MIM; 154360; -.
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                                                             TRANSMEM
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MEDLINE=98112863; PubMed=9446624;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANUFACTURING.

CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
linked D-glucose residues with release of D-glucose.

CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the ch
with release of beta-D-glucose.

SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O J. 6:2891-2896(1987).

FUNCTION: MAY SERVE AS AN ALTERNATE PATHWAY FOR STARCH DIGENEED LONGLED BECAUSE OF WHEN LUMINAL ALPHA-AMYLASE ACTIVITY IS REDUCED BECAUSE OF IMMATURITY OR MALMUTRITION. MAY PLAY A UNIQUE ROLE IN THE DIGESTION OF MALTED DIETARY OLIGOSACCHARIDES USED IN FOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: SULFATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYD
SIMILARITY: CONTAINS 2 P-TYPE (TREFOIL) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE II MEMBRANE TISSUE SPECIFICITY: EXPRESSED IN SMALL KIDNEY BUT NOT IN SALLVARY GLAND OR PAN PTM: N- AND O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                           PS00129; GLYCOSYL_HYDROL_F31_1; PS00025; P_TREFOIL; 1.
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                                                           Repeat;
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                                                                                                                    Transmembrane; Glycoprotein; gnal-anchor; Sulfation.
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15-JUL-1998 (Rel. 36, C
15-JUL-1998 (Rel. 36, L
16-OCT-2001 (Rel. 40, L
STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
MEDLINE-98037514; PubMed-9371463;
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
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                                                                                                                                                                                                                                                                                              between
the Euro
                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 396:133-140(1998).

-!- FUNCTION: REQUIRED FOR CORRECT LOCALIZATION OF PRECURSOR PROTEINS BEARING SIGNAL PROTIDES WITH THE TWIN ARGININE CONSERVED MOTIF S/T-R-R-X-F-L-K. THIS SEC-INDEPENDENT PARHWAY IS TERMED TAT FOR TWIN-ARGININE TRANSLOCATION SYSTEM. THIS SYSTEM MAINLY TRANSPORTS PROTEINS WITH BOUND COFACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATA_RICPR STANDARD; PRT; 54 AA 692CJI.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-MAR-2002 (Rel. 41, Last annotation updat sec-independent protein translocase protein
TATA OR RP749.
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                                                  Transport; Protein transport; Translocation;
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InterPro; IPR003369; MttA_Hcf106.
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                                                                              Pfam; PF02416; MttA_Hcf106;
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NCBI_TaxID=782;
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PROSITE; PS00527; RIBOSOMAL_S14; 1.
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                                                                                                                                                                                                                                                                                                                                                reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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IAPP_FELCA P12967;
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                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
SEQUENCE
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PIR; A33542; A33542.
PIR; B26619; B26619.
InterPro; IPR001693; Calc_CGRP_IAPP.
InterPro; IPR000443; Islet_amyloid.
Pfam; PF00214; Calc_CGRP_IAPP; 1.
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SM00113; CALCITONIN; 1.
E; PS00258; CALCITONIN;
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KRandler D., Ebner C., Prillinger H., Kraft D., I
"Molecular cloning of major and minor allergens
alternata and Cladosporium herbarum.";
Mol. Immunol. 32:213-227(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota Pleosporales; Pleosporaceae; MCBI_TaxID=5599;
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"Genome sequence of the
Buchnera sp. APS.";
Nature 407:81-86(2000).
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Bacteria; Proteobacteria;
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STRAIN=08-0203-BERLIN;
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60S acidic ribosomal protein Pl (Allergen Alt
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Pfam; PF01386; Ribosomal_L25p; 1.
ProDom; PD012503; Ribosomal_L25p; 1.
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Schizosaccharomyces pombe.";
Mol. Gen. Genet. 191:519-524(1983).
Mol. Gen. Genet. AN IMPORTANT ROLE
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Sequence of the cDNA for one acidic ribosomal protein

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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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60S acidic ribosomal protein P2-alpha (A2)
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Nucleic Acids Res. 15:9089-9089(1987)
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MISCELLANEOUS: YEASTS CONTAIN 4 INDIVIDUAL SMALL RIBOSOMAL A
PROTEINS (RPA) WHICH CAN BE CLASSIFIED INTO TWO COUPLES OF SIMILAR
BUT NOT IDENTICAL SEQUENCES. EACH COUPLE IS DISTINCTLY RELATED TO
ONE OF THE TWO A PROTEINS PRESENT IN MULTICELLULAR ORGANISMS.
MISCELLANEOUS: RPA3 AND RPA4 ARE ESSENTIAL FOR CELL SURVIVAL,
WHEREAS RPA1 AND RPA2 ARE NOT.
   SIMILARITY:
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E
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                        RPA4
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                       HIGHLY RELATED
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AC OSYSW9
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DT 16-OCT
DE 50S ri
GN RPL12P
OS Aeropy
OC Acropy
OC NCBLIN
RN ISBULIN
RN ISBULIN
RN KAWATA
RA HOSOYA
RA KAWATA
RA HOSOYA
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Best Local
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MEDLINE-99310339; PubMed-10382966;

Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,

Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,

Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,

Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,

Nakamura Y., Nomura N., Sako Y., Kikuchi H.;

"Complete genome sequence of an aerobic hyper-thermophilic

crenarchaeon, Aeropyrum pernix KI.";

DNA Res. 6:83-101(1999).

DNA Res. 6:83-101(1999).

THE BINDING SITE FOR SEVERAL OF THE FACTORS

-!- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS
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Q9Y9W9;
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or send a
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30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                           Pfam; PF00428; 60s_ribosomal; 1.
                                                                                                                EMBL; AP000063; BAA81181.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50S ribosomal protein RPL12P OR APE2170.
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Ribosomal protein; Phosphorylation; Multigene family.
SEQUENCE 110 AA; 11158 MW; 2B465A46E51606FE CRC64;
                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aeropyrum pernix.
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                                                                                                                                                                   an email to license@isb-sib.ch).
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                                                                                         IPR001813;
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Ribosomal protein;

Complete proteome

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2330740B03C6412A CRC64;

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                                                                                                                                                                                                                                                                                                                         Ribosomal
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tweedie S., Charlton J., Clark V., Bird A.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP (
PROTEIN SYNTHESIS.
-i- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                            EMBL; Z83263; CAB05855.1; -.
Interpro; IPR001813; 60s_ribosomal.
Pfam; PF00428; 60s_ribosomal; 1.
                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
60S acidic ribosomal protein P2.
Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota, Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
Ig heavy chain V-I region HG3
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SEQUENCE FROM N.A. MEDLINE=83144028; PRechavi G., Ram D.,
                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                           HV1B_HUMAN
P01743;
                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
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116 AA;
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 PubMed=6298778;
., Glazer L., Zakut
                                                                                                                                                                                                                                                                                                                     Phosphorylation.
11557 MW; 39C16854F10DC00C CRC64;
                                                           Chordata;
Primates;
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100.0%;
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TO THE L12P FAMILY OF RIBOSOMAL PROTEINS
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                                                                                            precursor.
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  Givol
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                                                                                                                                                                                                                          "Genome sequence C.

Buchnera sp. APS.";

Nature 407:81-86(2000).

NATURE 407:81-86(2000).

PINCTION: INVOLVED IN THE GO SYSTEM RESPONSIBLE FOR REMOVING AN OXLDATIVELY DAMAGED FORM OF GUANINE (7,8-C)LHYDRO-8-OXCOUANINE)

FROM DAM AND THE NUCLEOTIDE POOL. 8-OXO-DCTP IS INSERTED OPPOSITE DA AND DC RESIDUES OF TEMPLATE DNA WITH ALMOST EQUAL EFFICIENCY
THUS LEADING TO A.T TO G.C TRANSVERSIONS. MUTT SPECIFICALLY
DEGRADES 8-OXO-DGTP TO THE MONOPHOSPHATE (BY SIMILARITY).
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InterPro; IPR00396; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE ..... STRAIN-TOKYO 1998;
STRAIN-TOKYO 1998;
MEDLING-20445173; PubMed=10993077;
MEDLING-20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mutator mutT protein (7,8-ddhydro-8-oxoguanine-triphosphatase)
(8-oxo-dGTPase) (EC 3.6.1.-) (dGTP pyrophosphohydrolase).
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SUBUNIT: MONOMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The general mitochondria.";
Nature 396:133-140(1998).
-I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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PROSITE; PS00893; NUDIX; 1
Mutator protein; DNA replication; DNA repair; Hydrolase; Magnesium;
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Eriksson A.-S., Winkler
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Andersson S.G.E.,
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T., Alsmark U.C.M., Podowski R.M.,
inkler H.H., Kurland C.G.;
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P55047;
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"""rosinase co-factor (URF402).
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01-FEB-1996
Photosystem
                                                                                        "The chloroplast genome of a chlorophyll a+
Odontella sinensis.";
Plant Mol. Biol. Rep. 13:336-342(1995).
-!- FUNCTION: PSAD CAN FORM COMPLEXES WITH
OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I)
-!- SIMILARITY: BELONGS TO THE PSAD FAMILY.
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STRAIR-AFCC 13032 / ETH 22794 / GLA.0;
STRAIR-B8040431; PubMed=3118334;
MEDLINE-88040431; PubMed=3118334;
Huber M., Huetter R., Lerch K.;
"The promoter of the Streptomyces glaucescens mel operon."
Nucleic Acids Res. 15.8106-8106(1987).
-I- EUNCTION: THIS PROTEIN MAY FUNCTION TO DELIVER COPPER
                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                             SEQUENCE
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Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Kowallik K.V., Sto
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2839;
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Tada N., Otsuka S., Oyaizu H., Matsumoto S.;
"Plastid DNA sequences of Skeletonema costatum NIES 323.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FOXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.
-!- SIMILARITY: BELONGS TO THE PSAD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,

RO Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,

Yamada M., Yasuda M., Tabata S.,

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01-FEB-1991 (Rel. 17, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Photosystem I reaction center subunit II (Photosystem I 16
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"Molecular cloning and sequencing of the psaD gene encoding subunit I of photosystem I from the cyanobacterium, Synechocystis sp. PCC
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Nakazaki N., Naruo K.,
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                                                                                                                                                                                                           Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
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Pfam; PF02531; PsaD; 1.
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                                                              B, exbB and exbD genes.";
Microbiol. 24:169-179(1997).
FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT
TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILAR SUBUNIT: THE ACCESSORY PROTEINS EXBB AND EXBD SEEM TO FOR COMPLEX WITH TONB (BY SIMILARITY).
                             COMPLEX WITH TONB (BY SIMILARITY).
SUBCELLULAR LOCATION: Type II membrane protein (Probable).
SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.
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15-DEC-1998 (Rel. 37, Last sequence upda
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Biopolymer transport exbb protein.
EXBD OR NMA1983 OR NMB1728.
Neisseria meningitidis (serogroup A),
Neisseria meningitidis (serogroup B), an
Neisseria meningitidis (serogroup C).
Bacteria; Proteobacteria; beta subdivisi
                                                                                                                                                                                    Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davles R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quall M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXBD_NEIMA
P95376;
15-DEC-1998
        Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty I Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                 SEQUENCE FROM N.A.
STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                                                                                                                      STRAIN-8013.6 / SEROGROUP C;
MEDLINE-97158676; PubMed-9006036;
Stojiljkovic I., Srinivasan N.;
"Neisseria meningitidis tonB, exbB, and
utilization of protein-bound iron in Nei
J. Bacteriol. 179:805-812(1997).
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SEQUENCE
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16-OCT-2001
16-OCT-2001
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Science 287:1809-1815(2000).

-:- FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).

-:- SUBUNIT: THE ACCESSORY PROTEINS EXBB AND EXBD SEEM TO FORM A COMPLEX WITH TONB (BY SIMILARITY).

-:- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (Probable).
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                                                                                                                                             MEDLINE-20445173; PubMed-10993077; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishika "Genome sequence of the endocellular bacterial symbiont Buchnera sp. APS."; Nature 407.81-86(2000).
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Bacteria; Proteobacteria;
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                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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16-OCT-2001 (Rel. 40, Last annotation update)
16.7 kDa protein in whiE locus (WhiE ORF II
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09fnt2 beta vulgar
019762 caenorhabdi
097wn5 sulfolobus
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09ha66 homo sapien
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O96exz homo sapien
O9fft78 arabidopsis
O98eg1 rhizobium 1
O9sbi8 hordeum vul
O43488 hordeum vul
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O9vv71 drosophila fas
O9pc11 xylella fas
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O9pc160 triticum ae
O61288 arabidopsis
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O99tc4 homo sapien
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O99tc4 rhizobium 1
O91c2 arabidopsis
O17854 caenorhabdi
O95h24 arabidopsis
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Q9ha18 homo sapien
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Q9fn23 arabidopsis
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Ia Watanabe S., Kimura M., Murakami K., Murakami K., Murakami K., Murakami K., Murakami K., Nurakami K., Murakami K.
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09HA66;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                      PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 4.
PROSITE; PS00678; WD_REPEATS_1;
PROSITE; PS50082; WD_REPEATS_2;
PROSITE; PS50294; WD_REPEATS_REG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Q9Z7U4;
01-MAY-1999
                                                                                                                                                                                                                                                                          Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumo from Japan and CWLO29 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
-- SIMILIARITY: TO ATPASE ALPHA/BETA CHAINS FAMILY.
EMBL; AE002175; AAD18749.1; --
EMBL; AE002175; AAF38020.1; --
EMBL; AE002175; BAA98817.1; --
EMBL; AP002547; BAA98817.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99206606; PubMed-10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fa Olinger L., Grimwood J., Davis R.W., Stephens R.S "Comparative genomes of Chlamydia pneumoniae and Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae (Chlamydophila pneumoniae) Bacteria; Chlamydiales; Chlamydiaceae; Chlamydop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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InterPro; IPR002059; Cold_shock.
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Best Local S
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A Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget
A Domann E., Dominguez-Bornal G., Duchaud E., Durant L., Dussurget
A Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson
A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell
A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Tecopparative genomics of Listeria species.";
Query Match
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Q92DD2;
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01-DEC-2001 (TrEMBLrel. 19,
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Bacteria; Firmicutes; Bacillus/Staphylococcus
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                     "Comparative genomics of Listeria Science 294:849-852(2001).
EMBL, AL596166; CAC96114.1; -.
ListiList; LINO0882; -.
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X MEDLINE=20222556; PubMed=10761919;

A Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C. A. Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T., A. Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Hol A. Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Hol Jagels K., Leather S., Moule S., Mungall K., Quail M.A., A Jagels K., Leather S., Moule S., Mungall K., Quail M.A., A Whitehead S., Spratt B.G., Barrell B.G.;

T "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";

L Nature 404:502-506(2000).

R EMBL; AL162752; CAB83583.1; -.

R HSSP; P00959; 1MEA.
[1]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed=7906398;
Wilson R., Ainscough R., Anderson F
Wilson R., Burton J., Connell M.
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                                                                                                                                                                                                                                                                                                                                                                                     Q23635
Q23635;
Q1-NOV-1996
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ZK84.1 PROTE
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01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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InterPro; IPR002304; tRNA-synt_met.
InterPro; IPR002547; tRNA_bind.
Pfam; PF01588; tRNA_bind; 1.
PRINTS; PR01041; TRNASYNTHMET.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                 NCBI_TaxID=6239;
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                                    Anderson K. Connell M.,
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red. No. 10;
Mismatches
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                                       Coulson
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Randell M.D., Zhang O., Chen L.X.,
RA George R.A., Lewis S.E., Randell M.D., Zhang O., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Ballew R.M., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier R., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davanport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Doubtin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kalush P., Laing Y., Lilang Y., Lilang Y., Lilang Y., Lilang Y.,
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01-MAY-2000 (TrEMBLrel. 13,
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MEDLINE=20196006;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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Submitted (APR-1995) to the EN
EMBL; U23181; AAC48204.1; -.
SEQUENCE 801 AA; 77123 MW;
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EMBL/GenBank/DDBJ
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A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Sylerskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Sylerskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
A Zhus S.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL, AEOU3827, AAF58716.1; -.
BR EJBL; AEOU3327, AAF58716.1; -.
BR EJBL; AEOU33231.
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01-JUN-2001 (
PROBABLE 50S
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Nature 407:508-513(2000).
EMBL; AL445064; CAC11502.1;
InterPro; IPR001813; 60s_ribosomal.
Pfam; PF00428; 60s_ribosomal; 1.
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MEDLINE-20479972;
MEDLINE-20479972;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Ruepp A., Graml W., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasm.
acidophilm.";
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L 15.4 KDA PROTEIN.
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J. Biol. Chem. 273:6030-6040(1998).

EMBL; U33059; AAC13999.1;

InterPro; IPR004359; HATPase_C.
InterPro; IPR004359; HIS_KIN_sig.

Pfam; PF02518; HATPase_C; 1.
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                                      AIDS
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Taylor M., Hoffmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98174059;
August P.R., Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            units in ansamycin pathway.":
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Actinosynnemataceae
                                                                    STRAIN-PO1;
                                                                                                          Viruses;
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Transmembrane
          Pfam;
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                                               "Phylogenetic analysis of circulating
                                                          Heredia A.;
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                                                                                                 NCBI_TaxID=11709;
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Viruses; Retroid viruses;
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L., Yoon Y.J., Ning S., Mueller
nn D., Kim C.G., Zhang X., Hutchi
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Q9FNT2;
Q1-MAR-2001
01-MAR-2001
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Q39133;
01-NOV-1996
01-NOV-1996
01-DEC-2001
MAJOR LATEX
                                Beta vulgaris (Sugar beet).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core el

Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta

NCBI_TaxID=3555;
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SEQUENCE
STRAIN-CV. R
Fowler M.R.,
                                                                                                                                                                                                                                                         ripening-induced proteins.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ EMBL; X91961; CAA63027.1; -
EMBL; AJ306138; CAC83602.1; -
SEQUENCE 155 AA; 17879 MW; 61DC38712D035CF
                                                                                                                                                                                                                                                                                                 STRAIN-COL-0;
Muller S., Klimt S., Hauser M.T.;
"Molecular and phylogenetic analysis of a chaliana with similarities to major latex,
                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 STRAIN-COL 0;
Grellet F., C
                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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Similarity 100.0%;
7; Conservative
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REGINA; TISSUE-STORAGE ., Gartland J., Norton V
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(TIEMBLrel. 01, Last sequence update)
(TIEMBLRel. 19, Last annotation update)
PROTEIN TYPE3 (MAJOR LATEX-LIKE PROTEIN).
                                                                                                                                  PRELIMINARY;
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Pred. No. 31;
0; Mismatches
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Pred. No. 30;
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"Genome sequence ...
investigating biology.";
Science 282:2012-2018(1998).
Science 274472; CAA88941.1; -.
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Q19762;
Q1-NOV-1996;
Q1-NOV-1996;
Q1-DEC-2001;
SEQUENCE FROM N.A.

STRAIN-ATCC 35092 / DSM 1617 / P2;

MEDLINE-21332296; PubMed-11427726;

She Q., Singh R.K., Confalonieri F., Zivanovic Y

Awayez M.J., Chan Weiher C.C.-Y., Clausen I.G.,

De Moors A., Erauso G., Fletcher C., Gordon P.M.

Heikamp-de Jong I., Jeffries A.C., Kozera C.J.,
                                                                                                                                                 Sulfolobus solfataricus Archaea; Crenarchaeota; NCBI_TaxID=2287;
                                                                                                                                                                                                                                            01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scott N.W.;

*RS2:a sugar beet gene related to the latex-allergen Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databas EMBL; AJ278989; CAC18641.1; -.

SEQUENCE 158 AA; 16099 MW; 12DFB67F1AF439AO CRC64
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Submitted (JUN-1996)
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llarity 100.0%;
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Q96EX2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO HYPOTHETICAL PROTEIN FLJ14627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9RW97;
Q9RW97;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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"The com
Proc. Na
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MEDIINE=20036896; PubMed=10567266;
MEDIINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Moffat K.S., Qin H., Jiang L., Utterback T., Zalewski C.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R
Makarova K.S., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 286:1571-1577(1999).
EMBL; AE001932; AAF10355.1;
TIGR; DR0772; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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Charlebois R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete SEQUENCE 219 AA; 22631 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the radioresistant bacterium radiodurans R1.";
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                                                                                                                                                                                                                                                                                                                                                                                            GTPAPAA
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1 (TrEMBLrel. 16, 1
hL 22.6 KDA PROTEII
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PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; DB 1
Pred. No. 42;
0; Mismatches
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Pred. No. 36;
0; Mismatches
                                            Craniata; Vertebrata; Catarrhini; Hominidae;
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72AD261C8B37AB2F
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36;
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                                                                  Euteleostomi;
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Best Loc
Matches
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Best Loc
Matches
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01-0CT-2001
01-0CT-2001
                SEQUENCE FROM N.A.
STRAIN-MAFF303099;
MEDLINE-21082909; PubMed-11214968;
MEDLINE-21082909; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamo Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ da
EMBL; BC011878; AAH11878.1; -.
SEQUENCE 231 AA; 25722 MW; B4D36B036OD3C57C
                                                                                                                                                                                                                                                                                                                                                       exist in plants.";

Submitted (NOV-2000) to the

EMBL; AJ297951; CAC16575 1;

SEQUENCE 241 AA; 25455 MY
                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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TISSUE=MUSCLE, AND
                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                        Rhizobium
                                                                                                                                                             MLL4259
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01-MAR-2001
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  Mesorhizobium
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          "Complete
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Similarity 100.0%;
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genome structure
bium loti.";
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Last annotation update)
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          nitrogen-fixing
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. 44;
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                                                                                                                               Rhizobiaceae
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          symbiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          eudicots;
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                                              Sasamoto imura T.,
                                                                                                                                                                                                                                                                                                                                                                                              receptors
                                                                                                                               group;
          bacterium
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RESULT QSPA4 ID SSPA4 AC QSPA4 AC QSPA4
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Best Local S
Matches 7
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Best Local S
Matches
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Q9SPA4;
Q1-MAY-2000
01-MAY-2000
01-JUN-2001
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Q9SBI8;
01-MAY-2000
01-MAY-2000
01-JUN-2001
DEHYDRIN 8.
                                                                                                                                                                                                                           Hordeum vulgare (Barley).
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vannoliophyta; Liliopsida; Poales; Poaceae; Pooides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN 1998) to the EMBL/GenBank/DDBJ database: EMBL; AF043093; AA002259.1; -.
InterPro; IPR000167; Dehydrin.
Pfam; PF00257; dehydrin; 2.
PROSITE; PS00823; DEHYDRIN_2; 2.
SEQUENCE 255 AA; 27726 MW; 08D7FAFF7F811A4F CRC64;
                                                        STRAIN-CV. MOREX;
Choi D.-W., Close T.J.;
                                                                                                                                                                                                                                                                                                                                             DHN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. DICKTOO;
Choi D.-W., Zhu B., Close T.J.;
"The barley (Hordeum vulgare L.) dehydrichromosome assignments, and expression of cv. Dicktoo.";
Submitted (JAN-1998) to the EMBL/GenBar
      "Morex
family.
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EMBL; AP003003; BAB50958.
Complete proteome.
SEQUENCE 249 AA; 27855
                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Es
Spermatophyta; Magonliophyta; Liliopsida;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHN8
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                         DEHYDRIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206
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      barley (Hordeum
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100.0%;
                                  vulgare
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Last
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Last annotation update)
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Pred. No
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Pred. No.
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ession characteristics of 11
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                                  CV.
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. 47;
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a; Poales; Poaceae; Pooideae;
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                               multigene
                                                                                                                                                                                                                                                 Pooideae;
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1 dhn genes
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Best Local S
Matches 7
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                            dehydration stress.",
Plant Sci. 105:71-80(1995).
EMBL; X84056; CAA58875.1; ...
InterPro; IPR000167; Dehydrin.
Pfam; PF000257; dehydrin; 2.
PROSITE; PS00823; DEHYDRIN.2; 2
SEQUENCE 255 AA; 27666 MW; 4
                                                                                                                  09VV71
09VV71;
01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q43488;
Q43488;
SEQUENCE FROM N.A.
STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A.,
                                                         Eukaryota; Metazoa; Arthropoda;
Pterygota; Neoptera; Endopterygo
Ephydroidea; Drosophilidae; Dros
                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                NCBI_TaxID=7227;
                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. GEORGIE;
Grossi M., Gulli M.,
                                                                                                           CG4229
                                                                                                                                                                                                                                                                                                                                                             "Characterization of two
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             Triticeae; Hordeum.
NCBI_TaxID=4513;
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Pfam; PF00257; dehydrin; 2.
PROSITE; PS00823; DEHYDRIN.2;
SEQUENCE 255 AA; 27670 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF181458; AAF01696.1; -.
                                                                                                                                                                                                                            149 PAPAAEE
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                                                                                                                                                                                                         PAPAAEE
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                                                                                                         PROTEIN (LD44179P).
                                                                                                                                                                                                                                             7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                  (TrEMBLrel. 13, (TrEMBLrel. 19,
                                                                                                                                      (TrEMBLrel. 13,
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                            155
                                                                                                                                                                                                         212
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=GREEN LEAF;
                                                                                                                                                                                                                                                      3.0%;
                                                        Endopterygota; Diptera;
ilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%;
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two barley
                                                                                       (Fruit
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19,
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Last
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Last sequence
Last annotation
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                                                                                                                                      Created)
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Pred. No. 48;
0; Mismatches
                                                                                                                                                                                                                                                      Score 7; D
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5289E18CB420BF3B
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49C4618BC95A77FD CRC64;
                                                                                                                                                          PRT;
                                                                                      fly)
                                                                             Tracheata;
                                                                                                                                                                                                                                              Mismatches
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annotation update)
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48;
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                                                                             Hexapoda;
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                                                                   Brachycera;
                                                                                                                                                                                                                                                                Length 255
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                                                                             Insecta;
                                                                    Muscomorpha;
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Evans

C.A.,

Gocayne J.D.,

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RESULT
Q9PD13
ID Q0
AC Q0
DT 00
DT 00
DT 00
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Yellams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Yellams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Yellams S.M., Nusseri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

"The genome sequence of Drosophila melanogaster.";

RN Cibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                    Matches
               Q9PD13
Q9PD13;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          YU C. Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AE003527; AAR49451.1; --
EMBL; AY061476; AAL29024.1; --
ETyBase; FBgn0036639; CG4229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Ağbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N
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                                                                                                                                                                                           APAAEET
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                                                                                                                                                                                                                                                                  Similarity 7; Conser
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IPR004019; YLP.
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) (TremBLrel. 15, () (TremBLrel. 15, I) (TremBLrel. 19, I (TremBLrel. 19, I PROTEIN XF1591.
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Wortman J.R., Yan,
Rogers Y.-H.C., 1
1e C., Baxter
                                                                                                                                                                                                                                                                    Conservative
                                                                                             PRELIMINARY;
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5.
27418
                                                                                                                                                                                                                                                                                  3.0%;
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                                                                                                                                                                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                                                                ; Score 7; DB 5;
%; Pred. No. 48;
0; Mismatches
                 Created)
Last sequence update)
Last annotation updat
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Qy
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RA Simpson A.J.G., Reinach F.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.B.A., Carraro D.M., Carrer H.
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Krieger J.E., Kuramae E.E., Laigret T., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret L., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Manques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Monto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Monto B.R., Pereira G.A.G., Pereira H.A. Jr., Salvaski H.E.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Solveia M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Jusuka M.A.,
RA de Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Jusuka M.A.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RM Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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Best Local S
Matches 7
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01-OCT-2000 (
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01-DEC-2001 (
HYPOTHETICAL
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.
                                                                                      STRAIN=9A5C;
MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                  XF1697
                                                                                                                                                                                                                                                                                                                                             Q9PCT1
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                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                   Xylella fastidiosa
                                                                                                                                                             NCBI_TaxID=2371;
                                                                                                                                                                                Xylella
                                                                                                                           SEQUENCE
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0 (TrEMBLrel. 15,
1 (TrEMBLrel. 19,
AL PROTEIN XF1697.
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                               gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1; Pred. No. 48; 0; Mismatches
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Last annotation updat
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E38B51EFDDD82010
                                                                                                                                                                                               subdivision; Xanthomonas group;
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RX MEDILINE-20365717; PubMed=10910347;

RX Almpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

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RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Carrer H.,

RA Coutin N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

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Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

RA Manchado M.A., Nascimento A.L.T.O., Netto L.E.S.,

Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,

RA Meloto B.R., Pereira G.A.G., Pereira H.A. Jr., Paris A.,

Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Paris A.,
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RA FACINCANIA R.P., FERREITA W.C.A., PERTO J.A.,

RA FRAGINCANIA R.P., FERREITA W.C.A., PERTO J.A.,

RA FRAGINATION R.P., FERREITA W.C.A., PERTO J.A.,

RA GARINER M., GOLdman G.H., GOLdman M.H.S., Gomes S.L., Gruber A.,

RA GARINER M., GOLdman G.H., GOLdman M.H.S., Gomes S.L., Gruber A.,

RA GARINER M.C., KURAMAE E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

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RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

RA Moon D.H., Nagai M.A., Nascimento M.L.T., Sawasaki H.E.,

RA Moon D.H., Nagai M.A., Nascimento M.L.T., Sawasaki H.E.,

RA Menck C.F.M., Mobrega F.G., Nunes L.T.O., Netto R.A.,

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RA Menck C.F.M., Mobrega F.G., Silva W.A., Jr.,

RA Menck C.F.M., Mobrega F.G., Silva W.A., Jr.,

RA Menck C.F.M., Mobrega F.G., Silva W.A., Jr.,

RA Menck C.F.M.
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Best Local :
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-9A5C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
L PROTEIN XF2765.
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56 AA; 27871 MW;
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Pred. No.
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S., Ferreira V.C.A., 1
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283DDA924DD82015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subdivision; Xanthomonas group;
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48;
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Query Match
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Best Local Similarity
7; Conser
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01-MAY-1997 (TreMI
01-DEC-2001 (TreMI
COLD ACCLIMATION I
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-v. Danyluk J., Sarhan F.;
Danyluk J., Sarhan F.;
"Identification of a gene encoding an acidic d
"Identification of a gene encoding an acidic d
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
Submitted (OCT-1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
"The genome sequence of the plant pathogen Xylella fastidiosa."; RMBL, AE004082; AAF85550.1; "EMBL, AE004082; AAF85550.1; "EMBL, AE004082; AAF85550.1; "EMBL, AE004082; AAF85550.1; "".
               Arabldopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                             01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                  T14P8.5 PROTEIN.
T14P8.5 OR AT4G02450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnoliophyta;
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                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. NORSTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WCOR410C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P93608;
                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                   210 PAPAAEE 216
                                                                                                                                                                                                                                            149 PAPAAEE 155
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                                                                                                                                                                                                                                                                                                                                nitted (v. 177)

L; U73211; AABH8202.1; -.

erPro; IPR000167; Dehydrin.

m; PF00257; dehydrin; 2.

NSITE; PS00823; DEHYDRIN_2; 2.

NIFNCE 259 AA; 27945 MW;
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(TrEMBLrel. 03, Last sequence update)
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ATION PROTEIN WCOR410C.
                                                                                                                                                    PRELIMINARY;
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yta; Liliopsida;
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9B9A45D96AA05961 CRC64;
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a; Poales; Poaceae; Pooidea
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Mayer K.F.
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STRAIN-CV.
                                                                                            Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Conson R., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Farsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
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Submitted
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SEQUENCE
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                  Nature 368:32-38(1994).
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V. COLUMBIA;
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COLUMBIA;
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Caenorhabditis.
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Pred. No
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Best Local
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Waterston R.;
Submitted (MAY-1997) to t
EMBL; U42844; AAB53817.1;
SEQUENCE 263 AA; 30460
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01-MAY-1999
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                         Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Triticeae; Triticum.
NCBI_TaxID=4565;
                                                                                   01-MAY-1997 (TrEMBLrel. 03, Create 01-MAY-1997 (TrEMBLrel. 13, Last s 01-DEC-2001 (TrEMBLrel. 19, Last c 01-DEC-2001 (TrEMBLrel. 19, Last c 00LD ACCLIMATION PROTEIN WCOR410B.
                                                                                                                                                                                                                                                                      Localization in Rhodobacter sphaeroides Genetics 153:525-538(1999).
EMBL; AF108766; AAD09126 1; -
SEQUENCE 266 AA; 27988 MW; D45992B6B
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MEDLINE-99442363; PubMed-10511537;
MACKENTALE C., Simmons A.E., Kaplan S.;
Multiple Chromosomes in Bacteria: The Yin and Yang
"Multiple Chromosomes in Bacteria: The Yin and Yang
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Bacteria; Pı
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Proteobacteria;
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"Identification of a gene encodi:
Submitted (OCT-1996) to the EMBL,
EMBL; U73210; AAB18201.1; -.
InterPro; IPR000167; Dehydrin.
Pfam; PF00257; dehydrin; 2.
PROSITE; PS00013; DEHYDRIN_2; 1.
SEQUENCE 268 AA; 28837 MW; B
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DNA Res. 7:331-38(2000).
EMBL; APO03009; BAB52809.1; -.
InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp; 1.
Complete proteome.
SEQUENCE 272 AA; 29561 MW; 7B0
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Bacteria; Proteobacteria; alpha subdivision;
Phyllobacteriaceae; Mesorhizobium.
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"Mycobacterium bovis BCG clone E4863."; submitted (JUN-1997) to the EMBL/GenBanl EMBL; AF009829; AAB63811.1; Interpro; IPR0022965; P_rich_extensn. PRINTS; PR01217; PRICHEXTENSN.
Hypothetical protein.
Hypothetical protein
                Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=358;
                                                   Agrobacterium tumefaciens Plasmid Ti.
                                                                                                                                                                                                                                                                                       Submitted (JUL-2001) to the EMEMBL; AF397166; AAL04088.1; -. SEQUENCE 299 AA; 32725 MW;
                                                                                                                                                                                                                                                                                                                         "Novel sucrose-dependent mutans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=BCG FRENCH; Kim J.K., Choe Y.K.;
                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans. Bacteria; Firmicutes;
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            L., Tanzer J.M.;
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                                                                                                                                                                                                                                    Similarity 7; Conserv
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GTrEMBLrel.
(TrEMBLrel.
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Pred. No. 54;
0; Mismatches
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                                        Rhizobiaceae group;
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Best Local
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Q9BVC4;
Q9BVC4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO G BETA-LIKE PROTEIN (HYPOTHETICAL 35.9 KI
                                                                                                                                                                             PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
PROSITE; PS50082; WD_REPEATS_2; 3.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; WD repeat; Hypothetical protein.
SEQUENCE 326 AA; 35876 MW; 43A600D4EF2B6543
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Mol.
[2]
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Submitted (NOV-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg
Submitted
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TISSUE=PLACENTA, CHORIOCARCINOMA;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Octopine-type Ti plasmid sequen
Submitted (MAR-2000) to the EMBL
EMBL; AF242881; AAB88473.1; -
InterPro; IPR000515; BPD_transp.
                                                                                                                                                                                                                                                                                     PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 6.
                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: CONTAINS 6 WD EMBL; BC001313; AAH01313.1; -. EMBL; BC017119; AAH17119.1; -. EMBL; BC017119: DR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Winans S.C., : Farrand S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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Lyi S.M., Jafri S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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"Mannopinic acid and agropinic acid
type Ti plasmid pTi15955.";
Mol. Microbiol. 31:339-347(1999).
                                      142
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ш
                                    MNTSPGT 148
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7; Conserv
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                                                                                Conservative
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Primates;
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Pred.
                                                                                                 Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                           Mismatches
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59;
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AC Q0
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"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO2753; BAB55182.1;
SEQUENCE 330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q96SU5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seque)
01-DEC-2001 (TrEMBLrel. 19, Last annot.
CDNA FLJ14627 FIS, CLONE NTZRP2000289.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Tucker C.S., Hirono I., Aoki T.;

Tucker C.S., Hirono I., Aoki T.;

"Molecular cloning of CCAAT/enhancer binding proteins in flounder Paralichthys olivaceus, a first report of C/EBP Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AB049813; BAB49971.1;

InterPro, IPR001871; bZIP.

SMART; SM00338; BRLZ; 1.

SEQUENCE 346 AA; 39086 MW; 2772CF80D59BEC05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paralichthys olivaceus (Flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CCAAT/ENHANCER BINDING PROTEIN BETA.
JFC/EBPB.
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Q98TD7;
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Q9JY60;
01-OCT-2000
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ISOGAI T., Ota T., Hayashi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                             09JY60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8255;
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                                                                                                                                                                                                                                                      7; Conserv
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ilarity 100.0%;
Conservative (
(TrEMBLrel.
                                             PRELIMINARY;
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X MEDLINE-2022255; PubMed-10761919;

A Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C. A. Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., A. Davies R.M., Davies P., Devlin K., Feltwell T., Hamlin N., Hol A. Davies R.M., Davies P., Devlin K., Feltwell T., Quail M.A., A. Davies R.M., Simmonds M., Skelton J., A. Pajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., A. Whitchead S., Spratt B.G., Barrell B.G.;

T "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";

L Mature 404:502-506(2000).

R EMBL; AL162757; CAB85197.1;

R InterPro; IPR00345; CytC_heme_bind.

R InterPro; IPR00318; CytC_CIC.

R InterPro; IPR00319; Cyt_CIC.

R Pfam: pF000345; cyt-CIC.
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Best Local
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EMBL; AE002522; AAF42068.1; -.

TIGR; NMB1723; -.

InterPro; IPR000345; CytC_heme_bind.

InterPro; IPR003088; Cyt_CI.

InterPro; IPR003229; Cyt_CIC.

Pfam; PF00034; cytcohrome_C; 2.

PRINTS; PR00605; CYTCHROMECIC.

PRINTS; PR006190; CYTOCHROME_C; UNKNOWN_1.
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O9JT44;

O9JT44;

O1-OCT-2000 (TrEMBLre
O1-DEC-2001 (TrEMBLre
O1-DEC-2001 (TrEMBLre
PUTATIVE CYTOCHROME C
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01-DEC-2001
CYTOCHROME C
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MEDLINE-2017575; PubMed-10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E. Cotton M.D., Utterback T.R., Khourl H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Gill J., Scarlato V., Masignani W., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis (son Bacteria; Proteobacteria; NCBI_TaxID=491;
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Bacteria; Proteobacteria; beta sul
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(TrEMBLrel. 19, Last annotation update)
C OXIDASE, SUBUNIT III.
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Pred. No.
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subdivision;
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SEQUENCE FROM N.A.
MEDLINE-99184957; PubMed-10082609;
MEDLINE-99184957; PubMed-10082609;
MEDLINE-99184957; PubMed-10082609;
Minus Properties of the pheasants ("A molecular phylogeny of the pheasants ("Ineages are not monophyletic.";
                                                                                                                                                        01-NOV-1998
01-NOV-1998
01-DEC-2001
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EMBL; AB016064; BAA31583.1; -.

ITNEETPTO; IPR001993; Mitoch_carrier.

Pfam; PF00153; mitoch_carrier.

PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.

SEQUENCE 366 AA; 38658 MW; 7A372332D8D416CE CRC64;
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PROSITE;
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
MITOCHONDRIAL PHOSPHATE TRANSPORTER.
                                                                                           Archosauria; Aves;
                                                                                                     Eukaryota; Metazoa;
                                                                                                                          Pucrasia macrolopha
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                                                                      NCBI_TaxID=9061
                                                                                  Pucrasia
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C -i- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
C RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
C COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
C -i- COPACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
C BOUND TO THE PROTEIN (BY SIMILARITY).
C -i- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
C -I- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
C -I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
C -I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR PROBLE; APO28800; PAC62190.1; -
DR Pfam; PPO0033; CYTOCHROME_B_C: 1.
DR PFam; PPO0033; CYTOCHROME_B_HEME; 1
DR PROSITE; PS00193; CYTOCHROME_B_HEME; 1
DR PROSITE; PS00193; CYTOCHROME_B_BO; UNKNOWN_1.
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Matches 7
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01-MAY-2000
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor.
Bacteria; Pirmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                         MEDLING-9/, VICTOR MEDLING-9/, WILLIAM MEDLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2);
Thomson N.R., Parkhi
Submitted (NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver K., Harris D.;
Submitted (NOV-1999)
                                                                                                                                                                                                                                                                                                                                           the 8 mb Streptomyces coelicolor mol. Microbiol. 21:77-96(1996). EMBL; AL132856; CAB60469.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9RK28
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                                          146
                                                                                                                                                                                                                                                                               Hypothetical protein SEQUENCE 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299
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                                          PGTPAPA
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                                                                                                         Similarity 7; Conserv
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 13, Last annotation update)
L 42.3 KDA PROTEIN.
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                               42349 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barrell B.G., Rajandream M.A.; e EMBL/GenBank/DDBJ databases.
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                                                                                                         0;
                                                                                                                                         Score 7; I
                                                                                                                                                                                                                                                                               A21C43451BE4AB92 CRC64;
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                                                                                                         Mismatches
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                                                                                                                       DB
69;
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ID OPEUM3
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Query Match
Best Local
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01-AUG-1998
01-JUN-2001
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058434;
                                                                                                                                                                                         "Characterization of a Novel Cysteine Proteinases from Fi Submitted (DEC-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Naga Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguc Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
                                                                                   InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site
Pfam; PF00112; Peptidase_C1; 1.
                                                                                                                                                                                                                                Guiliano D.B., Blaxter "Characterization of a
                                                                                                                                                                                                                                                                                                                      Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda;
Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP000003; BAA29794.1; --
InterPro; IPR002665; MgtE.
Pfam; PF01769; MgtE; 2.
Hypothetical protein; Complete
SEQUENCE 397 AA; 43585 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota;
NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL 43.6 PH0703.
                               PROSITE; PS00139; THIOL_PROTEASE_CYS; PROSITE; PS00639; THIOL_PROTEASE_HIS;
                                                                                                                                                           EMBL; AF331036; AAK16514.1; HSSP; O17473; 1BMU.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus horikoshii.
                Hydrolase;
                                                                      PRINTS; PR00705; PAPAIN.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                                                                                             CATHEPSIN L-LIKE CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9вJM3;
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                                                                                                                                           MEROPS; C01.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 VLLIVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 VLLIVEV
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 401 AA;
                Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.0%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
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45511 MW;
                                                                                                                                                                                                               M.L., Williams S.A., I
Novel Developmentally
rom Filarial Nematodes
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                                                                                                                                                                                                                                                                                                                                                                             PROTEINASE
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                                                                                                                                                                                                                                                                                                                                                                                            Last sequence up
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                                                                                                                                                                                               EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; |
Pred. No.
                                                                                                                                                                                                                                                                                                                                            Chromadorea;
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FD4B7456F42FBBA6
58E10CE3913A3F66 CRC64;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
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on update)
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                                                                                                                                                                                                                                                   Lustigman
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                                                                                                                                                                                               databases
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                                                                                                                                                                                                                                    Family
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffalli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffalli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Wilming L.,
RA Hayashiawa Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RENE M. Masegawa Y., Kawaji H., Kohtsuki S.,
RA RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 7
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-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROT
EMBL; AKO18378; BAB31185.1; -
MGD: MGI:87937; Adrb1
InterPro; IPRO00276; GPCR_Rhodpsn.
InterPro; PRO00017, 7tm_1 1.
Pfam; PF000017, 7tm_1 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-Protein coupled receptor; Glycoprotein; Tra
NON_TER
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01-JUN-2001 (TrEMBLrel. 17, 0
01-JUN-2001 (TrEMBLrel. 17, 1
01-JUN-2001 (TrEMBLrel. 17, 1
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Mus musculus (Mouse).
Mus musculus (Mouse).
"" Metazoa; Chordata;
"" heria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-C57BL/6J; T
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Sequence features of the regions of 1,191,918 bp covered
T physically assigned pl clones.";
L DNA Res. 4:401-414(1997).
R EMBL; AB007644; BAB10733.1; -.
R Interpro; IPR000219; DAG_PE-bind.
R Interpro; IPR000215; Serpin.
R Interpro; IPR000215; Serpin.
R SMARF; SM00109; C1; 4.
R PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
R PROSITE; PS500284; SERPIN; UNKNOWN 1.
SEQUENCE 419 AA; 48481 MW; B38F1A57A45645C5 CRC64;
                                                                             "Genome sequence of the nematode investigating biology."; Science 282:2012-2018(1998). EMBL; 293381; CAB07607.1; -. SEQUENCE 450 AA; 52757 MW; 49
                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                          017854
017854;
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnolliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
SIMILARITY TO CHP-RICH ZINC FINGER PROTEIN.
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                                                                                                                                           none;
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MEDLINE=99069613;
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                                                                                                                                                                                                              SEQUENCE
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Tabata S.;
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S., Kaneko T.,
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Pred. No.
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Q9H7M8;
O1-MAR-2001 (TrEMBLrel. 16, Cr
O1-MAR-2001 (TrEMBLrel. 19, La
O1-DEC-2001 (TrEMBLrel. 19, La
FLJ00042 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                       Q9AY47 PRELIMINARY; PRT; 458 AA.
Q9AY47;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE NUCLEIC ACID BINDING PROTEIN.
QSJNBA0027P10.
                                                                                                          SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE;

Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Hsiao J.,

Zismann V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E., Craven B.,

Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                        "Oryza sativa chromosome 10 BAC OSJNBa0027P10 Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; ACO84763; AAG60186.1; -. InterPro; IPR004087; KH. TYPE_1. InterPro; IPR004088; KH_TYPE_1. Pfam; PF00013; KH-domain; 3. SMART; SM00322; KH; 3.
                                                                                                                                                                                                      Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AK024450; BAB15740.1; -. InterPro; IPR001806; Ras_trnsfrmng. InterPro; IPR003575; Small_GTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
MCBI_TaxID=9606;
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SMART; SM00010; small_GTPase; 1.
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TISSUE-SPLEEN;
  SEQUENCE
              PROSITE;
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Similarity 100.0%;
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PS50084; KH_TYPE_1; 3
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Pred. No. 79;
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Search completed: August 13, 2002, 08:42:13
Job time: 231 sec